

For Reference

NOT TO BE TAKEN FROM THIS ROOM

Ex LIBRIS
UNIVERSITATIS
ALBERTAENSIS





Digitized by the Internet Archive
in 2019 with funding from
University of Alberta Libraries

<https://archive.org/details/Soomro1974>

THE UNIVERSITY OF ALBERTA

A BIOMETRICAL-GENETIC ANALYSIS OF SOME QUANTITATIVE CHARACTERS

IN A FIVE-PARENT DIALLEL CROSS OF COMMON WHEAT

(*TRITICUM AESTIVUM* L.)

by



BARKAT ALI SOOMRO

A THESIS

SUBMITTED TO THE FACULTY OF GRADUATE STUDIES AND RESEARCH

IN PARTIAL FULFILMENT OF THE REQUIREMENTS FOR THE DEGREE

OF DOCTOR OF PHILOSOPHY

DEPARTMENT OF GENETICS

EDMONTON, ALBERTA

SPRING, 1974

To Mäntaaz Khàtoon Soomro.

ABSTRACT

Common wheat (*Triticum aestivum* L.) cultivars Marquis, Chinook, Khush-hal, Ciano-67 and Inia-66 were used as parents of a five-parent diallel cross. The F_1 , F_2 , backcross and selfed backcross generations of this diallel cross were used as materials in this study. The experimental data were investigated by means of principal factor analysis, general and specific combining ability analysis, diallel cross analysis for genetic components of variation and genotype-environment interaction analysis. The data on ten characters were recorded from materials grown at Ellerslie and Parkland. The characters considered were: onset-of-heading, final heading, heading-span, plant height, number of tillers per plant, number of spikelets per spike, number of seeds per spike, weight of seeds per spike, 1000-kernel weight and yield per plant.

In the factor analyses, correlation matrices indicated that early maturing varieties were high yielding. Yield per plant was positively correlated with its subcharacters or components. There was no correlation between yield and plant height. Varimax rotated factor matrices for each generation of the diallel cross constituted five principal factors which were named according to the magnitude of the factor loading on the characters. The results of the factor analyses confirmed the conclusions drawn from correlation analyses. The scores of factor loadings on various characters were different for two locations but the generations appeared not to affect them significantly.

The general and specific combining ability analyses indicated that parental lines possessing high GCA's usually produced hybrids with low SCA's and therefore general combining ability of the parents does not necessarily constitute a criterion for evolving hybrids with high specific combining ability. The variances for GCA's were usually greater than those for SCA's for all the characters, and in those cases where SCA-variances were larger, the importance of non-additive gene effects for the characters concerned has been emphasized. SCA-variances significantly higher than GCA variances indicated instabilities of the cultivar for the character concerned and therefore these differences may be used as criteria for the selection in pedigree-record breeding. Mean squares for GCA's were in general all significant. Analysis also showed that GCA's were not significantly affected either by generations of the diallel set or by locations. The stability of the response of each cultivar with respect to its GCA was consistent over two locations.

The mean degree of dominance with respect to different characters ranged from partial to over-dominance. The proportions of alleles with positive and negative effects were not the same for all the characters: complete symmetry was observed for some and asymmetry for others. For some characters dominant and recessive genes in the parents were in equal proportions and for others either there was a preponderance of dominants or of recessives. Character differences were found to be controlled by at least one to three groups of genes. The analyses for the characters considered have shown that

the genetic components of variation were relatively stable over the generations. They were more consistent when estimated from the variances and covariances of adjusted treatment means (from *ANOVA* of partially balanced lattice design) than when estimated from unadjusted means (experiments treated as randomized blocks).

ACKNOWLEDGEMENTS

I wish to express my sincere appreciation to Dr. Rüstem Aksel for guiding the project. His formative criticism and invaluable suggestions gave this manuscript a final shape. Painstaking editing without demur, of the draft by Dr. G.W.R. Walker is gratefully acknowledged.

Seed of Pakistani and Mexican introductions was obtained through the courtesy of (Late) Mr. B.G. Shaikh, wheat Botanist, Agricultural Research Station, Dera Ismail Khan, Pakistan, and Dr. Norman E. Bourlaug of CIMMYT, Mexico, respectively.

The author is also grateful to Dr. K.G. Briggs and Mr. J.E. Fitzsimmons of the Department of Plant Science, The University of Alberta, for lending a piece of land at Parkland Farm and extending full facilities for seeding the replicated trial. Voluntary help in seeding the experimental material and weeding the plots by Messrs. Bruce Hobin, Peter Vermier, Peter Conway and my colleagues in the Department of Genetics is gratefully appreciated. Mrs. Neli Farolan typed my thesis for which I am indebted to her.

The author's stay in Canada was under the auspices of Government of Canada, through the Commonwealth Scholarship and Fellowship Administration. Financial support by them for the present studies deserves a special note of gratitude.

TABLE OF CONTENTS

	Page
ABSTRACT	iv
ACKNOWLEDGEMENTS	vii
LIST OF TABLES	ix
LIST OF FIGURES	xviii
LIST OF APPENDICES	xxvi
INTRODUCTION	1
REVIEW OF LITERATURE	4
MATERIAL AND METHODS	19
EXPERIMENTAL RESULTS	28
Analysis of F_1 data	28
Analysis of F_2 data	68
Analysis of backcross data	107
Analysis of selfed backcross data	145
Analysis of genotype-environment interaction	180
DISCUSSION	199
BIBLIOGRAPHY	210
APPENDICES	223

LIST OF TABLES

Table	Page
1. Mean-square values from the analysis of variance of partially balanced triple lattice design with respect to ten characters at two locations	29
2. Simple correlation coefficients between ten characters from F_1 diallel set at two locations	31
3. Varimax rotated factor matrix for ten characters from F_1 diallel set at two locations	33
4. Estimates of general combining ability of five parental lines used in F_1 diallel set for ten characters at two locations	35
Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F_1 diallel set at two locations for:	
5. Onset-of-heading	37
6. Final heading.	37
7. Heading-span	39
8. Plant height	39
9. Number of tillers per plant	40
10. Number of spikelets per spike	60

Table	Page
11. Number of seeds per spike	41
12. Weight of seeds per spike	41
13. 1000-kernel weight	42
14. Yield per plant	42
15. Analysis of variance of general and specific combining ability for ten characters from F_1 diallel set at two locations	44
16. Mean squares from the analysis of variance of the 5 x 5 F_1 diallel table for ten characters at two locations.	46
17. Analysis of variance of $W_r - V_r$ differences for ten characters from F_1 diallel set at two locations	48
18. Estimates of second degree statistics parameters for ten characters from F_1 diallel set at two locations	50
19. Estimates of components of variation for ten characters from F_1 diallel set at two locations	51
20. Proportional values of the estimates of genetic parameters for ten characters from F_1 diallel set at two locations	53
21. Simple correlation coefficients between ten characters from F_2 diallel set at two locations	64

Table	Page
22. Varimax rotated factor matrix for ten characters from F_2 diallel set at two locations	71
23. Estimates of general combining ability of five parental lines used in F_2 diallel set for ten characters at two locations	74
Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F_2 diallel set at two locations for:	
24. Onset-of-heading	76
25. Final heading	76
26. Heading-span	77
27. Plant height	77
28. Number of tillers per plant	79
29. Number of spikelets per spike	79
30. Number of seeds per spike	80
31. Weight of seeds per spike	80
32. 1000-kernel weight	82
33. Yield per plant	82

Table	Page
34. Analysis of variance of general and specific combining ability and reciprocal effects from F_2 diallel set for ten characters at two locations	84
35. Mean squares from the analysis of variance of 5 x 5 F_2 diallel set for ten characters at two locations	85
36. Analysis of variance of $W_r - V_r$ from F_2 diallel set for ten characters at two locations	86
37. Estimates of second degree statistics parameters for ten characters from F_2 diallel set at two locations	86
38. Estimates of genetic components of variation from F_2 diallel set at two locations	88
39. Proportional estimates of genetic parameters for ten characters from F_2 diallel set at two locations	89
40. Arrangement of backcrosses and reciprocals in which the parents of rows are kept as recurrent parents . . .	108
41. Arrangement of backcrosses and reciprocals in which the parents of columns are kept as recurrent parents . .	108
42. Simple correlation coefficients between ten characters from backcross diallel set at two locations	110

Table	Page
43. Varimax rotated factor matrix for ten characters from backcross diallel set at two locations	112
44. Estimates of general combining ability of five parental lines used in backcross diallel set at two locations	115
Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from backcross diallel set at two locations for:	
45. Onset-of-heading	117
46. Final heading	117
47. Heading-span	118
48. Plant height	118
49. Number of tillers per plant	120
50. Number of spikelets per spike	120
51. Number of seeds per spike	121
52. Weight of seeds per spike	121
53. 1000-kernel weight	122
54. Yield per plant	122

Table	Page
55. Analysis of variance of general and specific combining ability and reciprocal effects for ten characters from backcross diallel set at two locations	123
56. Mean squares from the anlysis of variance of 5 x 5 backcross diallel set for ten characters at two locations	125
57. Analysis of variance of $W_r - V_r$ for ten characters from backcross diallel set at two locations	126
58. Estimates of second degree statistics for ten characters from backcross diallel set at two locations	126
59. Estimates of genetic components of variation from backcross diallel set for ten characters at two locations	128
60. Proportional estimates of genetic parameters from the backcross diallel set for ten characters at two locations	129
61. Simple correlation coefficients between ten characters from a selfed backcross diallel set at two locations	146
62. Varimax rotated factor matrix for ten characters from a selfed backcross diallel set at two locations.	148

Table	Page
63. Estimates of general combining ability for five parental lines used in selfed backcross diallel set at two locations	150
Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from selfed backcross diallel set at two locations for:	
64. Onset-of-heading	152
65. Final heading	152
66. Heading-span	153
67. Plant height	153
68. Number of tillers per plant	155
69. Number of spikelets per spike	155
70. Number of seeds per spike	156
71. Weight of seeds per spike	156
72. 1000-kernel weight	157
73. Yield per plant	157
74. Analysis of variance of general and specific combining ability and reciprocal effects from selfed backcross diallel set at two locations . . .	159

Table	Page
75. Mean squares from the analysis of variance of 5 x 5 selfed backcross diallel set at two locations	161
76. Analysis of variance of $W_r - V_r$ for ten characters from selfed backcross diallel set at two locations	162
77. Estimates of second degree statistics for ten characters from selfed backcross diallel set at two locations	162
78. Estimates of genetic components of variation for ten characters from selfed backcross diallel set at two locations	164
79. Proportional estimates of genetic parameters for ten characters from selfed backcross diallel set at two locations	165
80. Factorial analysis of variance of factor loadings of varimax-rotated factor matrices of F_1, F_2 , backcross and selfed backcross diallel sets over two locations	181
81. Factorial analysis of variance of general combining ability over four generations and two locations	183
82. Analysis of variance of Parkland GCA's regression upon Ellerslie for each of the parental lines	185

Table	Page
83. Factorial analysis of variance of genetic components of variation over generations and locations	187
84. Analysis of variance of regression of genetic components of variation of Parkland upon those of Ellerslie for each generation	189
85. Components of genetic variation obtained from statistics based on adjusted treatment means for ten characters over four generations at two locations	191
86. Estimates of genetic parameters from diallel analysis of adjusted treatment means for ten characters over four generations at two locations	193
87. Analysis of variance of regression of genetic componenets of variation at Parkland upon those at Ellerslie averaged over generations for all characters	195
88. Summary of the results of general and specific combining ability analyses showing that hybrids with highest SCA's are associated with parents of low GCA's	203

LIST OF FIGURES

Figure	Page
1. W_r, V_r graph for onset-of-heading from F_1 diallel set	54
2. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for onset-of heading from F_1 diallel set	54
3. W_r, V_r graph for final heading from F_1 diallel set	56
4. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for final heading from F_1 diallel set	56
5. W_r, V_r graph for heading-span from F_1 diallel set	57
6. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for heading-span from F_1 diallel set	57
7. W_r, V_r graph for plant height from F_1 diallel set	58
8. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for plant height from F_1 diallel set	58
9. W_r, V_r graph for number of tillers per plant from F_1 diallel set	60
10. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of tillers per plant from F_1 diallel set	60
11. W_r, V_r graph for number of spikelets per spike from F_1 diallel set	62

12.	Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of spikelets per spike from F_1 diallel set	62
13.	W_r, V_r graph for number of seeds per spike from F_1 diallel set	64
14.	Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of seeds per spike from F_1 diallel set	64
15.	W_r, V_r graph for weight of seeds per spike from F_1 diallel set	65
16.	Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for weight of seeds per spike from F_1 diallel set	65
17.	W_r, V_r graph for 1000-kernel weight from F_1 diallel set	66
18.	Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for 1000-kernel weight from F_1 diallel set	66
19.	W_r, V_r graph for yield per plant from F_1 diallel set	67
20.	Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for yield per plant from F_1 diallel set	67
21.	W_r, V_r graph for onset-of-heading from F_2 diallel set	91
22.	Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for onset-of-heading from F_2 diallel set	91
23.	W_r, V_r graph for final heading from F_2 diallel set	92

Figure	Page
24. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for final heading from F_2 diallel set	92
25. W_r, V_r graph for heading-span from F_2 diallel set	94
26. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for heading-span from F_2 diallel set	94
27. W_r, V_r graph for plant height from F_2 diallel set	96
28. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for plant height from F_2 diallel set	96
29. W_r, V_r graph for number of tillers per plant from F_2 diallel set	98
30. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of tillers per plant from F_2 diallel set	98
31. W_r, V_r graph for number of spikelets per spike from F_2 diallel set	99
32. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of spikelets per spike from F_2 diallel set	99
33. W_r, V_r graph for number of seeds per spike from F_2 diallel set	100
34. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of seeds per spike from F_2 diallel set	100
35. W_r, V_r graph for weight of seeds per spike from F_2 diallel set	101

Figure	Page
36. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for weight of seeds per spike from F_2 diallel set	101
37. W_r, V_r graph for 1000-kernel weight from F_2 diallel set	102
38. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for 1000-kernel weight from F_2 diallel set	102
39. W_r, V_r graph for yield per plant from F_2 diallel set	104
40. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for yield per plant from F_2 diallel set	104
41. W_r, V_r graph for onset-of-heading from backcross diallel set	130
42. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for onset-of-heading from backcross diallel set	130
43. W_r, V_r graph for final heading from backcross diallel set	132
44. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for final heading from backcross diallel set	132
45. W_r, V_r graph for heading-span from backcross diallel set	133
46. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for heading-span from backcross diallel set	133
47. W_r, V_r graph for plant height from backcross diallel set	135

Figure	Page
48. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for plant height from backcross diallel set	135
49. W_r, V_r graph for number of tillers per plant from backcross diallel set	137
50. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of tillers per plant from backcross diallel set. .	137
51. W_r, V_r graph for number of spikelets per spike from backcross diallel set	138
52. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of spikelets per spike from backcross diallel set. .	138
53. W_r, V_r graph for number of seeds per spike from backcross diallel set	139
54. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of seeds per spike from backcross diallel set. . .	139
55. W_r, V_r graph for weight of seeds per spike from backcross diallel set	140
56. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for weight of seeds per spike from backcross diallel set. . .	140
57. W_r, V_r graph for 1000-kernel weight from backcross diallel set	141
58. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for 1000-kernel weight from backcross diallel set	141

Figure	Page
59. W_r , V_r graph for yield per plant from backcross diallel set	143
60. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for yield per plant from backcross diallel set	143
61. W_r , V_r graph for onset-of-heading from selfed backcross diallel set	166
62. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for onset-of-heading from selfed backcross diallel set	166
63. W_r , V_r graph for final heading from selfed backcross diallel set	167
64. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for final heading from selfed backcross diallel set	167
65. W_r , V_r graph for heading-span from selfed backcross diallel set	168
66. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for heading-span from selfed backcross diallel set	168
67. W_r , V_r graph for plant height from selfed backcross diallel set	170
68. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for plant height from selfed backcross diallel set	170
69. W_r , V_r graph for number of tillers per plant from selfed backcross diallel set	171

Figure	Page
70. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of tillers per plant from selfed backcross diallel set	172
71. W_r, V_r graph for number of spikelets per spike from selfed backcross diallel set	174
72. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of spikelets per spike from selfed backcross diallel set	174
73. W_r, V_r graph for number of seeds per spike from selfed backcross diallel set	175
74. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of seeds per spike from selfed backcross diallel set	175
75. W_r, V_r graph for weight of seeds per spike from selfed backcross diallel set	176
76. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for weight of seeds per spike from selfed backcross diallel set	176
77. W_r, V_r graph for 1000-kernel weight from selfed backcross diallel set	177
78. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for 1000-kernel weight from selfed backcross diallel set . .	177

Figure	Page
79. W_r , V_r graph for yield per plant from selfed backcross diallel set	178
80. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for yield per plant from selfed backcross diallel set	178
81. Regression of genetic components of variation at Parkland upon those at Ellerslie for all the characters except plant height	197

LIST OF APPENDICES

Appendix		Page
I	Origin, parentage and varietal description of five cultivars of wheat used in diallel study	223
II	Numerical designations of the parents and their crosses used in the diallel analyses	224
III	Onset-of-heading at Ellerslie	226
IV	Final heading at Ellerslie	227
V	Heading-span at Ellerslie	228
VI	Plant height at Ellerslie	229
VII	Number of tillers per plant at Ellerslie	230
VIII	Number of spikelets per spike at Ellerslie	231
IX	Number of seeds per spike at Ellerslie	232
X	Weight of seeds per spike at Ellerslie	233
XI	1000-kernel weight at Ellerslie	234
XII	Yield per plant at Ellerslie	235
XIII	Onset-of-heading at Parkland	236
XIV	Final heading at Parkland	237

Appendix		Page
XV	Heading-span at Parkland	238
XVI	Plant height at Parkland	239
XVII	Number of tillers per plant at Parkland	240
XVIII	Number of spikelets per spike at Parkland	241
XIX	Number of seeds per spike at Parkland	242
XX	Weight of seeds per spike at Parkland	243
XXI	1000-kernel weight at Parkland	244
XXII	Yield per plant at Parkland	245

INTRODUCTION

The degree to which a quantitative or metrical trait is phenotypically expressed in individuals depends on their genotype and the environmental conditions under which they are grown. It is assumed, and the experimental data seems to confirm it in most of the cases, that the genotype considered with respect to a metrical character is a set of genes referred to by Mather individually as polygenes and collectively as a polygenic system (Mather, 1949). These genes are often interdependent both in their action and transmission. In a polygenic system underlying a quantitative character, the allelic and non-allelic interactions are the most usual forms of manifestation of gene effects and inheritance pattern. The interaction of alleles at a given locus is known as dominance, while non-allelic interaction, viz., interaction between the genes at different loci, may take the form of complementary-gene, duplicate-gene or other classical relationships. All these effects are referred to generally as 'epistasis' in biometrical genetics.

Different genotypes defined with reference to a metrical character do not react alike to a given change in environment. This means that genotype and environment are not independent in their action in producing the phenotype. Consequently the variation in the degree of expression of the character is assumed to consist of genotypic, environmental and genotype-environment interaction components which may respectively be partitioned in a biometrically defined experimental design. The measurement of genotype-environment interaction in the diallel cross

is quite efficient and informative, since a number of parental strains can be assessed together with their hybrid generations.

The diallel cross technique is one of the conventional approaches used in biometrical genetics to obtain adequate information regarding the inheritance of a quantitative character. The procedure, first introduced by Schmidt (1919) involves crossing a set of parental lines in all possible combinations, including their reciprocals, in order to obtain an estimation of the magnitude of genetic variability ascribable to the differences among the parental lines. The quantitative genetic analysis of a diallel cross based on a set of postulated assumptions is presented and discussed in detail by Jinks and Hayman (1953), Hayman (1954a, 1954b, 1958 and 1960), Jinks (1954 and 1956) and Kempthorne (1956). By means of pertinent parameters obtainable from the analysis of the diallel cross, the mean degree of dominance, the proportion of positive to negative alleles at loci exhibiting dominance, the proportion of dominant to recessive genes in the parents, and the correlation between the parental order of dominance and parental measurements can be determined. In addition, the graphical analysis of the regression of array covariances (W_p) on array variances (V_p) permits the separation of true dominance from the spurious one caused by non-allelic interaction and categorizes the parents according to their degree of dominance.

The analysis of genotype-environment interaction by means of a diallel cross replicated in time, in space or in both time and space, provides information on the pattern of reaction of homozygous parents and their hybrids to environmental variation. The value of such an analysis

is that the significant inter-environmental differences characteristic of different genotypes are reflected in the array variances and covariances by their effects on the relative magnitude of components of these statistics. The project reported in this thesis deals with this type of analysis of genotype-environment interaction in a five-parent diallel cross in common wheat (*Triticum aestivum* L.). The purpose of the investigation was to obtain information regarding the extent to which the genetic components of variation and the combining abilities of the parental lines are affected by environmental changes.

REVIEW OF LITERATURE

General background

A diallel cross involves the mating of n genotypes, individual clones or homozygous lines in all possible combinations to give $[n(n-1)]$ crosses, including reciprocals. The total number of such combinations comes to n^2 if the parents are also included as selfs. The n^2 combinations may be arranged in the form of a square matrix, the rows and columns of which correspond to the offspring of each parent, the n parents themselves occupying the main diagonal. Such an arrangement of arrays, known as a diallel table, may be complete or incomplete. Complete tables consist of all n^2 entries, while in incomplete ones the parental or reciprocal entries may be absent. Griffing (1956) has developed four possible methods of constructing a diallel table, together with the corresponding forms of analysis. These are: (1) the parents, all the F_1 's and their reciprocals are included (n^2 combinations); (2) the parents and one set of F_1 's are included but not the reciprocals [$\frac{1}{2}n(n+1)$ combinations]; (3) one set of F_1 's and reciprocals are included but parents are not [$n(n-1)$ combinations]; and (4) one set of F_1 's is included but the reciprocal crosses and the parents are not [$\frac{1}{2}n(n-1)$ combinations]. For each of these combinations, Griffing has developed two kinds of statistical analyses, arising from different assumptions regarding the sampling nature of the experimental material; either it is assumed to be a random sample from the population or it is assumed to be deliberately chosen, and therefore not a random sample.

The biometrical-genetic analysis of a diallel cross as formulated by Hayman (1954b) is based on the following set of assumptions:

1. Homozygous parents
2. Normal diploid segregation
3. No differences between reciprocal crosses
4. Independent action of non-allelic genes
5. No multiple allelism
6. Genes independently distributed between the parents.

The genetic analysis, discussed by different authors (Hull 1945; Hayman 1954a, 1954b, 1958, 1960; Jinks 1954, 1956 and Jinks and Hayman 1953) implies the estimation of genetic components of variation from the following second degree statistics:

V_{OLO} = Variance of the parents

W_r = Covariance between the parents and their offspring in one array (r th. array)

W_{OLO1} = Mean covariance between the parents and their offspring over the arrays

V_r = Variance of the r th array

V_{1L1} = Mean variance of the arrays

$(M_{L1} - M_{LO})$ = Difference between the mean of the parents and the mean of their n^2 progeny

The description of the genetic components of variation is given below:

D = Component of variation due to additive gene effects

H_1 = Component of variation due to dominance effects of the genes

H_2 = Component of variation due to dominance effects, corrected for gene distribution

F = Covariation between additive and dominance effects over all the arrays. Thus F could be used to determine the relative proportion of dominant to recessive alleles in the parents involved.

The expected values of these genetic components of variation in terms of variances and covariances have been described by Mather (1949), Hayman (1954b, 1958), Jinks (1954, 1956) and Mather and Jinks (1971).

The relationship between the array variances and covariances, expressed graphically, shows the overall genetic situation with respect to the inheritance-pattern of a particular character. When the set of assumptions described earlier are valid, the $W_r - V_r$ differences are constant over the arrays, the regression of covariance on the array variance is a straight line of unit slope and all the points of W_r, V_r intercepts lie on this line. The upper and the lower limits where the W_r, V_r intercepts can lie are the points where the regression line intersects the limiting parabola. These points correspond respectively to the completely recessive and completely dominant parents, and thus show the possible limits of selection.

A deviation from the expected regression line of unit slope indicates the presence of non-allelic interaction. Any type of non-allelic interaction affecting the crosses in an array will inflate the variance of that array and reduce the parent-offspring covariance. Such an increase in variance relative to covariance will move the W_r, V_r graph towards the right, giving an apparent increase in dominance, and will cause the slope of the regression line to be less than unity. Thus, with $H_1 = D$ (complete dominance), $V_{1L1} \div W_{0L01} = 1$ and the line of unit

slope will pass through the origin; with $H_1 > D$ (over-dominance), $V_{1L1} \div W_{OL01} > 1$ and the line will cross the ordinate below the origin; and with $H_1 < D$ (partial dominance), $V_{1L1} \div W_{OL01} < 1$ and the regression line will pass above the origin. If, of course, $H_1 = 0$ there is no regression. The mean degree of dominance is measured by $(H_1 \div D)^{1/2}$. The ratio $(H_2 \div 4H_1)$ provides an estimate of the proportion of genes with positive and negative effects in the parents. The proportion of dominant to recessive genes in the parents is given by $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ and the number of groups of genes controlling the character and showing dominance can be determined by the formula $[h^2/H_2]$.

The failure of any one of the six postulated assumptions invalidates the analysis to a certain extent. The effects of the failure of these assumptions are discussed by Hayman (1954b). The methods of analysis of complete diallel tables as developed by Yates (1947), Hayman (1954a), Durrant (1965) and Jinks *et al* (1972) allow, among others, for the detection and testing of 'reciprocal differences'. Significance of the c pertaining to reciprocal differences in Hayman's analysis implies the expectation of two values for each of the genetic components of variation, D , H_1 , H_2 and F from the diallel table; one from the use of column arrays and the other from the use of row arrays. This ambiguity may be removed by replacing the off-diagonal cells of the diallel table by the common mean for the cross and its reciprocal. However, with significant c , the errors of the parameters will be inflated. Departure from independent action of non-allelic genes may be checked by examining

the $W_r - V_r$ values for homogeneity. Heterogeneity of $W_r - V_r$ differences indicates failure of the assumptions postulated. If this is the case, the inspection of the V_r, W_r graph would show which of the arrays contribute mostly to this failure. The disparate arrays may be eliminated, leaving a sub-diallel table for analysis that satisfies the null hypothesis. The results of the analysis would be valid, of course, for the remaining arrays.

Manifestations of 'non-allelic interaction', 'multiple allelism' and 'correlated gene distribution' introduce serious complications into the diallel analysis. They disturb the direction and mean degree of dominance, inflate the estimated proportion of dominant to recessive genes in the parents and reduce the estimate of the number of genes controlling a particular character. A test of homogeneity of variances of $W_r - V_r$ values has been advocated as an appropriate method for their detection.

Application of diallel cross analysis

The literature pertinent to diallel cross analysis as applied to plant breeding programmes is fairly impressive. In non-cereal crop plants, the technique has been widely used in the study of various quantitative characters. Thus this technique has been applied to brome grass (Knowles 1950; Greesom and Kalton 1956; Neilson and Kalton 1959; Dunn and Wright 1970), alfalfa (Kehr 1961; Theurer and Elling 1963a, b; Wilcox and Wilsie 1964), flax (Carnahan 1947; Durrant and Tyson 1964; Murty *et al* 1967; Anand and Murty 1968, 1969), cotton (Turner 1953; Marani 1963;

White and Richmond 1963; Marani 1964; Miller and Marani 1963; White and Kohel 1964), tobacco (Jinks 1954, 1956; Matzinger *et al* 1962; Marani and Sachs 1966; Povilaitis 1966; Legg *et al* 1970; Povilaitis 1970), strawberry (Morrow *et al* 1958; Aalders and Craig 1968; Watkins and Spangello 1968; Spangello *et al* 1971) and *brassica* (Johnston 1968a, b; Chiang 1969).

In cereals, a considerable number of studies using diallel analysis have been made with rice (Mohammad and Hanna 1965; Athwal and Singh 1966a, b; Wu 1968a, b; Cheng and Chang 1970), maize (Kinman and Sprague 1945; Sprague and Federer 1951; Bauman 1959; Matzinger *et al* 1959; Sprague 1964; Troyer and Hallauer 1968; Eberhart and Russell 1969; Poneilet and Bauman 1970), barley (Johnson and Aksel 1959; Aksel and Johnson 1961; Eunis *et al* 1962; Fasoulas and Allard 1962; Aksel and Johnson 1963; Johnson and Aksel 1964; Norington 1967, 1968; Persson 1969; Yap and Harvey 1971; Riggs and Hayter 1972, 1973) and *sorghum* (Chiang and Smith 1967a, b; Liang 1967; Liang *et al* 1968).

In wheat, the first report on the use of diallel analysis is that of Whitehouse and co-workers (1958). Of the five characters studied by them in a 4 x 4 diallel cross, viz., single kernel weight, grains per spikelet, spikelets per spike, ears per plant and yield per plant, all except yield per plant were found to be under additive genic control. For total yield, a generalized type of gene action was found in the F_1 but the F_2 generation exhibited a localized multiplicative type of gene action.

Lupton (1961) performed a diallel analysis of the yield of winter wheats. Though there was no non-allelic interaction (as revealed

by W_r , V_r graphs) in either the drilled or space-planted experiments, the position of the parents with respect to dominance was significantly changed in the two environments. The highest yielding parent, Capelle, exhibited dominance in the space-seeded trial and was reported to be the most recessive in the drilled trial. This change in yield inheritance was attributed to environmental differences of the inter-plant competition type which appeared to affect drill plantings more than space-seedings. In a later study (Lupton 1965), an incomplete diallel system, where reciprocals were excluded, was used to study the yield of spring wheat varieties replicated both in space and time, for F_1 , F_2 and F_3 generations. In all cases, interaction of over-dominance with site was highly significant, establishing consistency in the performance of the parents and their hybrid combinations.

Crumpacker and Allard (1962) analysed heading date in ten spring wheat varieties in a complete diallel test, replicated over three years. The results indicated substantial differences among the parents, generally categorized as highly dominant, moderately dominant, moderately recessive and highly recessive. The genetic system governing the maturation time of the parents, F_1 's and F_2 -generation hybrids consisted of a very few major genes showing dominance and was reported to be operating consistently in different years.

Fonseca (1965) studied the inheritance of yield and yield-components in a seven-parent diallel cross of wheat. The author reported significant differences among the parental lines used. The

graphical analysis revealed partial dominance to slight over-dominance for all the characters studied. Since all the F_1 's yielded higher than either of their respective parents, the author proposed a new term, heterobeltiosis, to describe the better performance of the F_1 over the better parent in the cross.

Bagnara (1967) performed a diallel analysis on normal and radiation-induced mutant lines of durum wheat. The results revealed significant differences between the lines and the mutants derived from them with regard to the expression of the degree of dominance. All the characters under study except spikelets per spike exhibited partial dominance.

Fonseca and Patterson (1968) studied hybrid vigour in a seven-parent wheat diallel to determine the diversity of germ-plasms in hill-planting experiments. The authors reported significant heterobeltiosis for yield and kernel-weight in half of the F_1 hybrids. The yield and kernel-weight estimates, were respectively 100% and 101 to 115% greater than either parent in hilled as against experimental nursery plots.

Walton (1969) studied the association of several morphological characters with yield in a seven-parent spring wheat diallel. He reported that the distance of the spike above the leaf-sheath at maturity and flag-leaf area were directly proportional to yield, and that yield, flag-leaf area and spike length were partially dominant.

Paroda and Joshi (1970) performed a genetic analysis of a complete 6 x 6 wheat diallel test for yield and its principal components: 1000-kernel weight, kernels per spike and tillers per plant. Yield and

1000-kernel weight exhibited non-allelic interaction of the duplicate-gene and complementary-gene type, respectively. For both characters, the variances for additive gene effects were significant.

Hsu and Walton (1970) studied gene action for yield and its components (spikes per plant, spikelets per spike, kernels per spike and 1000-kernel weight) in a 5 x 5 wheat diallel. For all the characters studied, the genetic variation was reported to be due to additive and dominance gene effects. Yield per plant exhibited complete, and its components partial, dominance.

Bitzer *et al* (1971) reported gene action and hybrid vigour in a six-parent wheat diallel. The results of two years of study revealed that the yield of the F_1 hybrids was not significantly higher than that of the parental strains. However, according to the graphical analysis of regression of W_r on V_r , plant height, kernel weight and spikelets per spike exhibited partial dominance while yield per plant showed over-dominance.

Kaltsikes and Lee (1971) estimated the genetic parameters for degree of dominance, ratio of total number of dominant to recessive parental genes and heritability for yield and its components in a 6 x 6 diallel of durum wheat. The average degree of dominance ranged from incomplete dominance to over-dominance and an excess of dominant over recessive alleles in the parents was found for all the characters studied. Since the heritability estimates for yield were as high as 61%, the authors suggested a pedigree selection procedure in breeding for yield characters in durum wheat.

General and specific combining ability

In quantitative genetics two types of combining ability, viz., general combining ability and specific combining ability are considered. General combining ability (GCA) refers to the average performance of a parental line as reflected in its hybrid combinations, while specific combining ability (SCA) refers to the performance of a particular cross. According to Sprague and Tatum (1942), GCA is due to genes which are largely additive, and SCA to genes showing non-additive effects. Nakamura (1956) considers GCA as 'an index of the number of effective genes' and SCA as 'an index of the number of common genes and the interaction between their alleles'. According to Fryxel *et al* (1958), GCA is the ability of a parental strain to produce promising or non-promising genotypes in its hybrids, regardless of the other parent involved, while SCA refers to this ability in hybrid combinations with certain other parental strains.

In a detailed examination of combining ability in the diallel cross, by Griffing (1956), eight procedures of statistical analysis have been proposed. These have been developed for four different diallel crossing schemes and for two alternative assumptions regarding sampling nature.

Kronstad and Foote (1964) using Griffing's diallel analysis for estimating GCA and SCA effects in ten winter wheat varieties found that a large portion of the total genetic variation for yield and yield components was associated with significant GCA effects. SCA effects were significant for yield per plant and plant height but not for yield components.

Fonseca (1965) studied the performance of F_1 hybrids for yield and yield components in a 7 x 7 diallel cross using Griffing's method 4 (one set of F_1 's is included in the diallel table but the reciprocal crosses and the parents are not) with fixed model. The results revealed that all the mean squares for GCA and some of the mean squares for SCA were significant.

Brown *et al* (1966) found that most of the variation in yield and other characters among F_1 wheat hybrids was associated with high GCA rather than with SCA variances.

Singh *et al* (1969) in an analysis of a 7 x 7 wheat diallel for combining ability and genetic parameters for yield and its components, reported importance of additive gene effects for general over the non-additive ones of specific combining ability for yield components. The variances for GCA and SCA in the case of yield were of the same order of magnitude, implying additive as well as non-additive effects.

Bhatt (1971) reported combining ability estimates for earliness, plant height and four yield components in a 5 x 5 wheat diallel. The analysis of GCA indicated that the larger portion of the genetic variation, for six out of seven characters considered, was associated with additive gene effects. The estimates of SCA's were highly significant but lower than GCA's for five characters.

Bitzer *et al* (1971) performed a combining ability analysis in a 6 x 6 diallel and found that GCA mean squares were significant for earliness, plant height and kernels per spike whereas SCA mean squares

were not. The average yield of the F_1 's was 28.1% higher than that of the highest yielding parent.

Paroda and Joshi (1970a) compared the combining ability variances of F_1 and F_2 generations for yield and other characters in a 6 x 6 wheat diallel. The GCA effects were high in the F_1 's and F_2 's but SCA effects were high only in F_1 's. Similar results were also reported by Niehaus and Pickett (1966) in a *sorghum* diallel.

In some of the papers it has been reported that the parents with high GCA values do not necessarily produce hybrids with high SCA values (Larson, 1941 in tomatoes; Crumpacker and Urquhart, 1962 in wheat; Walker 1963, Chang 1967, Soomro 1967, Baluch and Soomro 1969 and Soomro and Baluch 1969 in cotton). It follows, therefore, that the general combining ability should not be taken as a criterion for predicting high specific combining ability.

Genotype-environment interaction

Finlay and Wilkinson's (1963) regression analysis technique permitted for the first time a satisfactory assessment of the performance stability of a strain or cultivar over the range of environments in which it is grown. According to these authors, a regression of varietal-mean-yield on location-mean-yield with a regression coefficient of less than unity indicates that the variety has an above-average stability in its response to environmental influences. Regression coefficients equal to and greater than unity indicate average and less-than-average stability respectively. Eberhart and Russell (1966) interpreted stability in a

different manner, stating that the Finlay-Wilkinson model implies that a stable variety is one which performs relatively well in a poor environment and relatively poor in a favourable one. They proposed that the criteria for stability should be a regression coefficient of unity and minimum deviation from the unit slope. According to them a variety with high mean yield and fulfilling these two criteria would perform well in all the environments.

Another method of genotype-environment interaction analysis, in terms of biometrical genetics, has been developed by Bucio Alanis (1966) and applied to data for two inbred lines of *Nicotiana rustica* grown over a period of sixteen years at two locations. The analysis has shown that the effects of the genotype-environment interaction are linearly related to a particular environmental effect of the genotype. The model, which is essentially an extension of Mather's model (Mather, 1949), was later extended by Bucio Alanis (1966a) to apply to F_1 's with identical and consistent results for this generation also.

For the analysis of genotype-environment interaction by means of the diallel cross, three papers have appeared, one theoretical (Perkins, 1970) and two experimental (Allard, 1956; Crumpacker and Allard, 1962) and are concerned with assessing the stability of genetic components of variation under different environments.

Crumpacker and Allard (1962) studied genotype-environment interaction for heading date in a 10 x 10 wheat diallel over three years. The analysis of variance of heading time for parental genotypes indicated different additive and/or epistatic effects in different years. Because

of the homozygosity of the parents, the epistatic effects attributable to parents were defined by the authors as the result of interaction between homozygous loci, that is, additive x additive type of interaction. Stability of average degree of dominance was tested by the variance ratio for the dominance x year interaction. This was highly significant and showed that the mean degree of dominance for heading date varied from partial to complete dominance in consecutive years.

Porceddu (1968) in a yield test of three wheat varieties over twenty consecutive years at one location showed significant differences between varieties in different years. The results established that the performance of an individual genotype is a linear function of the environment, and that the major portion of the genotype-environment interaction could be accounted for by deviations from the linear response as estimated by the regression analysis.

Baker (1969), analysing the yield of six wheat varieties grown at nine locations over five years, subdivided the sum of squares for genotype-environment interaction into genotype x place, genotype x year and genotype x place x year interactions for each variety. Except for genotype x year, all interactions were highly significant, leading to the conclusion that the stability of performance of a particular cultivar over a range of environments is inversely proportional to the sum of squares for genotype-environment interaction for that particular variety.

Kaltsikes and Larter (1970) analysed genotype-environment interaction for height, maturity and yield in durum wheat. Five varieties

grown over four to five years at five loctions, differed with different environments in all the characters studied. In their analysis, the major portion of the genotype-environment interaction effects was reported to be linearly correlated with the environment.

A considerable amount of work has been reported on genotype-environment interaction analysis with respect to a variety of quantitative characters in different crops (Allard 1961, Parson and Allard 1960, Allard and Workman 1963, in lima-beans; Eagles 1967, Knight 1965, 1970 and Breese 1969, in grasses; Westerman 1970, 1971a, b, in *Arabidopsis*; Hill and Perkins 1969, Perkins and Jinks 1970, 1971a, b, in tobacco; Kaltsikes 1970, in winter rye; Liang and Walter 1966, in *sorghum* and Qualset 1968, and Paroda and Hayes 1957, in barley). In each of these papers, the behaviour of a particular genotype when grown in a particular environment, and when grown with other genotypes over a wide range of environments, is studied using linear regression analysis to measure the environmental effect. The implication of these studies is that the linear regressions of individual genotypic values on the mean values of all genotypes for each of the environments provide measures of the response that are useful in predicting the relative performance of the genotype in question over the range of environmental conditions. The conclusion of these reports focuses on one point: that the performance of an individual genotype in a particular environment is a linear function of the over-all environmental mean in regression analysis, where the slope of regression measures the sensitivity of the genotype to the totality of the environmental factors.

MATERIAL AND METHODS

Five cultivars of common wheat (*Triticum aestivum* L.)

described in Appedix I, were used in the diallel study. These varieties were selected on the basis of their diversity of origin, different spike and seed characteristics and their yield performances. The parental material was sown in September 1969 in the green-house to check its trueness to type. Fifteen to twenty phenotypically identical healthy heads were selected from each variety and their seed formed the basis of the present investigations. The parent lines were sown in the green house in January 1970. Crosses were made in all possible combinations, including reciprocals. During summer 1970, the parent material was again seeded at Parkland farm to obtain more F_1 seed. Following the winter, some of the F_1 seeds together with their parents were sown in growth chambers to make backcrosses, reciprocal backcrosses, further F_1 combinations and to provide F_2 seed. During 1971's spring the same procedure was repeated to have sufficient number of seeds for every combination. In the fall of 1971, the backcrosses and their reciprocals were seeded in the growth chambers to obtain seed for their first selfed generation.

By spring 1972, the experimental material consisted of five parents, 20 F_1 's, 20 F_2 's, 80 backcrosses and the selfed generation of these backcrosses, amounting to 205 different entries. A 15 x 15 partially balanced lattice design was chosen for seeding the material in a replicated trial. To meet the requirements of the design, 20 more entries were needed and since the F_2 is the maximum segregation generation,

each F_2 combination was represented twice in each replication to complete the required 225 entries. The names and numerical designations of the entries are given in Appendix II.. On 9th and 11th May, 1972, the whole of the experimental material was space-seeded in three replications at two locations, viz., Department of Genetics Ellerslie Field Lab. and Department of Plant Science Parkland Farm, respectively. Each of the fifteen (15' x 15') blocks in a replication consisted of 15 rows of 30 seeds each, with a spacing of 30.48 cm between rows and 15.24 cm between seeds within a row. The following observations were recorded at each of the locations:

- (1) Onset-of-heading: expressed as the number of days between seeding date and the date of appearance of the first head in the row (entry).
- (2) Final heading: recorded in number of days from the date of seeding to the day when 75% of the plants in a row have headed.
- (3) Heading-span: measured by the difference between (1) and (2).
- (4) Plant height: measured in centimeters from the surface of the soil to the tip of the spike on the highest tiller (excluding awns). Ten consecutive plants per row were recorded for height irrespective of their growth performance, leaving the first plant because of susceptibility to border effects, except in those rows where the number of surviving plants was reduced to ten or less. At maturity only those

plants that had been recorded for height were harvested. The following observations for yield and yield components were recorded on the harvested material.

- (5) Number of productive tillers per plant.
- (6) Number of spikelets per spike: Three spikes were taken at random from each plant and their spikelets counted.
- (7) Number of seeds per spike.
- (8) Weight of seeds per spike (in grams): spikes randomly sampled for spikelet-counts were threshed separately and their seeds counted and weighed.
- (9) 1000-kernel weight (in grams): computed from observations (7) and (8).
- (10) Yield per plant (in grams): expressed as total seed weight of all the spikes including those used for (6), (7), and (8).

Statistical analysis

The means were calculated for all the characters except onset-of-heading, final heading and heading-span. For observations (6), (7) and (8) means of three readings were calculated first and treated as individual variables for the calculation of entry means. Missing entries were calculated according to Cochran and Cox's (1957) formula for the randomized block design, except for (1) to (4) at Parkland. Here, since the number of missing entries was less than three, the procedure for the partially balanced lattice design was used. The complete set of data was subjected to analysis of variance for a partially balanced lattice design. This provided a single set of adjusted treatment means at each location. However, unadjusted treatment means (original entry

means as treated in randomized block design) were used for most of the analyses.. These were categorized into four diallel sets, viz., F_1 's, F_2 's, backcrosses and selfed backcrosses. The following analyses were performed on each of the sets for all the characters under study.

1. Correlation and factor analyses. Simple correlation coefficients were computed for each of the characters and arranged in the form of a matrix to permit the simultaneous comparison of one character with the other. Factor analysis was performed according to Hotelling's (1933) principal factor method as explained by Harman (1960) and Lawley and Maxwell (1963). The factor analysis approach aims at resolving the covariation into simpler relations in the form of a few factors which explain the larger portion of the variation in the original data. Statistically speaking, it reduces a large number of correlated variables to a small number of uncorrelated variables called factors, each of which proportionally accounts for the variability in the original observations.

The procedure for the principal factor method used in the present study was based on the following linear model (Harman, 1960):

$$z_j = a_{j1}F_1 + a_{j2}F_2 + \dots + a_{jm}F_m + d_j u_j \quad (j = 1, 2, \dots, n)$$

where z_j represents a character variable in terms of several underlying factors and each of the 'n' observed variables is described linearly in terms of 'm' common factors and the residual error ($d_j u_j$). The coefficients of these factors are referred to as factor loadings. A symmetrical correlation matrix produced from all possible $[1/2n(n - 1)]$ combinations is resolved into an 'nk' factor matrix, where the number of factors 'k' is usually smaller than 'n', the number of variables.

In the correlation matrix, the leading diagonal elements have values of unity and since they are meaningless (the correlation of each variable with itself means nothing) they are replaced by 'communalities' (the approximate values in terms of amount of variance accounted for by the common factors). In the present case the highest correlation value in each column of the correlation matrix was substituted for unity in the diagonal cells because the variance-covariance ratio of the column for that character is expected to be nearer to unity. With these communalities as the approximate values, the correlation matrix was factored by iteration to give a new resultant set of approximations to communalities that are more convergent. The factor matrix was then rotated (in this case by the varimax method) with every new set of communalities produced, till off-the-diagonal elements of the residual matrix were not significantly different from zero.

2. Combining ability analysis. General and specific combining ability analyses were performed following Griffing's (1956) method 1 (where all the n^2 entries of the diallel table are included), model 1 (where the experimental material is not regarded as a random sample from the population). Model 1 was chosen against model 2 (where the experimental material is regarded as a random sample from the population) because the parental lines, producing all the entries in the form of various combinations, were deliberately chosen on the basis of their diversity of origin and yielding capacities.

3. Diallel cross analysis. Diallel analysis was performed in two steps,

viz., diallel analysis for genetic components of variation and graphical analysis of regression of W_r (parent-offspring covariance of the r th. array) on V_r (variance of the r th. array) to complement the former via graphical representation. In the diallel analysis for genetic components of variation, each diallel table was subjected to tests of validity of the following assumptions (Hayman, 1954b):

- (1) Homozygous parents
- (2) Normal diploid segregation
- (3) No differences between the reciprocal crosses
- (4) No multiple allelism
- (5) Independent action of non-allelic genes
- (6) Uncorrelated gene distribution.

The condition of 'homozygous parents' in the present studies could be satisfied, as the parent material was sown preceding crossing and found to be true to type. 'Normal diploid segregation' may be assured from the pedigree-record of the organism used as experimental material. Wheat, though an amphi-diploid derivative of *Triticum monococcum* for the 'A' genome (Melburne and Thompson, 1927; Zohary and Feldman, 1962), *Aegilops speltoides* for the 'B' genome (Sarkar and Stebbins, 1956; Riley *et al*, 1958; Sears and Okamoto, 1958) and *Aegilops squarrosa* for the 'D' genome (Kihara, 1944; McFadden and Sears, 1944, 1946; Kihara and Lilienfeld, 1949) behaves cytogenetically as a normal diploid (Sears, 1948; Riley *et al*, 1961). It follows therefore, that, the assumption of normal diploid segregation could be considered valid. 'No reciprocal differences' were checked after Hayman's (1954a) procedure

of analysis of variance for diallel tables, where significance of the 'c' component indicates failure of this hypothesis. The remaining three conditions, 'no multiple allelism', 'independent action of non-allelic genes' and 'uncorrelated gene distribution' were checked through the analysis of variance of $W_r - V_r$ values for the arrays of each diallel table. Heterogeneity of $W_r - V_r$ variances will reveal non-validity of these assumptions.

After the validity checks for the above-mentioned conditions, the diallel analysis for genetic components of variation (Hayman 1954b, 1958 and Jinks 1954, 1956) was performed, on each of the diallel tables for all the characters under study, by replacing the off-diagonal cells of the diallel table with the common mean of the relevant cross and its reciprocal irrespective of the significance of Hayman's (1954a) 'c' component. In the F_2 -generation diallel, the estimates of genetic components of variation from the second degree statistics were computed after Johnson and Aksel's (1959) notation describing the average effect of Aa in different filial generations. According to their formula:

$$\text{effect of } Aa = [(1/2)^{fn-1} h]$$

where fn = nth filial generation

$$\text{thus in } F_2, \text{ effect of } Aa = [(1/2)^{2-1} h]$$

$$\text{and in } F_3, \text{ the effect of } Aa = [(1/2)^{3-1} h] \text{ and so on.}$$

From the genetic components of variation, various parameters such as the mean degree of dominance, the proportion of positive to negative alleles at loci exhibiting dominance, the ratio of dominant to recessive genes in the parents

and the number of groups of genes controlling the particular character were estimated. The heritability estimates were calculated after Crumpacker and Allard (1962) using the formula $[D \div (D + H_1 - F + 4E)]$.

The graphical analysis of regression of W_r on V_r was performed after Hayman (1954b) by plotting the regression line and the limiting parabola constructed by calculating its points ($W_r^2 = V_r \times V_{OLO}$) and plotting the V_r , $(W_r \times V_{OLO})^{1/2}$ points. The W_r , V_r graphs were supplemented with Johnson and Aksel's (1959) standardized deviation graphs of parental measurements (Y_r) and parental order of dominance ($W_r + V_r$) where the deviations of the Y_r 's and $W_r + V_r$'s from their respective means were standardized by dividing them by their respective standard deviations. An abscissa (Y_r) and an ordinate ($W_r + V_r$) intersecting each other produce four quadrants of the graph, classified as (+,+), (-,+), (-,-) and (+,-). The plus and minus signs for ($W_r + V_r$) denote 'recessive' and 'dominant' and for Y_r , they refer to 'high' and 'low' performances respectively.

4. Analysis of genotype-environment interaction. The constancy of principal factors with respect to loadings in four generations of diallel cross was studied by means of *factorial ANOVA* where locations, principal factors and generations were treated as main source of variation. The *ANOVA* was based on fixed-effect-model as described by Scheffe (1959) because the set of parents in all the diallel tables could not be regarded as random sample and the two locations at which the materials were grown could not be considered as representing

random sample of the environments. Their choice was dictated by the limitations imposed both by time and facilities available.

The differences between the two locations with respect to general combining ability were also studied by *factorial ANOVA*. Stability of each cultivar was determined by regressing its GCA at Parkland upon that at Ellerslie. The regression analysis used was as given by Mather (1951).

The genotype-environment interaction with respect to D , H_1 and F considered as variables was investigated by using factorial analysis of variance. The concordance of the components in the two locations was studied by regressing the values of D , H_1 and F estimated from Parkland data upon those of Ellerslie and partitioning the total sum of squares into sum of squares due to regression and due to deviation from regression (error). Diallel analysis for genetic components of variation from adjusted treatment means (balanced lattice design) was compared with that of unadjusted treatment means (experiment treated as a randomized block design). The differences between the parameter estimates would reflect the effect of the adjustment factor characteristic of partially balanced lattice design. The regression analysis (Mather, 1951) applied to D , H_1 and F obtained from both the adjusted and unadjusted treatment means, will reveal the degree of concordance between the parameters characteristic of each treatment.

EXPERIMENTAL RESULTS

The experimental data for the two locations; (1) Ellerslie and (2) Parkland, are given in Appendices III to XXII inclusive. Table 1 shows the results of the analysis of variance of the partially balanced lattice design and its efficiency as compared to the analysis as a randomized block. The mean squares of the adjusted treatments except for number of tillers per plant and yield per plant, both at Parkland, all showed significant differences among the entries. The relative efficiency of the balanced lattice design at Parkland over the randomized block design was greater than that at Ellerslie.

ANALYSIS OF F_1 DATA

Simple correlations were computed for all the characters under study and are given in Table 2. As shown in the table:

Onset-of-heading was positively correlated with plant height and number of spikelets per spike and negatively correlated with weight of seeds per spike and 1000-kernel weight at both locations. At Ellerslie, it was positively correlated with final heading and negatively with yield per plant, while at Parkland, it showed positive correlation with number of tillers per plant and number of seeds per spike. The negative correlation of onset-of-heading with yield, weight of seeds per spike and 1000-kernel weight indicates that the longer the period between seeding and the appearance of the first head for a particular entry, the lower will be its yield and 1000-kernel weight. Correlations of final heading and heading-span with other characters may be interpreted in the same fashion.

TABLE 1

Mean-square values from the analysis of variance
of partially balanced triple lattice design with respect to
ten characters at two locations

Character	Replication	Blocks within replications	Treatments (adjusted)	Error	Total sum of squares	% Efficiency over randomized block
†D.F.	2	42	224	406	674	
Onset-of-heading	5.7305 19.8980	4.9140** 18.1369**	10.3581** 18.2897**	1.0209 2.5313	2948.5180 5921.1450	119.205 127.013
Final heading	14.4640 204.9375	8.0242** 14.7080**	17.3218** 19.2502**	1.4999 3.1787	4849.0160 6601.6170	118.699 108.332
Heading-span	24.0635 137.0770	2.8539* 6.6719**	3.1996* 4.6495**	1.6111 2.6398	1532.3940 2662.3760	95.829 107.162
Plant height	273.8125 1017.5480	566.9384** 524.6927**	543.1358** 738.0608**	41.0030 129.1721	162503.6250 241583.5620	121.334 99.301
Number of tillers per plant	0.9950 133.0380	4.8374 10.5493**	4.6147 6.0799**	5.6567 3.0278	3495.9080 3288.2760	87.318 109.575
Number of spikelets per spike	10.8070 19.9485	2.5932** 4.1922**	1.8178* 2.2189**	1.3783 1.0273	1087.8420 1125.9980	85.553 109.766
Number of seeds per spike	10.0065 180.0355	50.2140** 36.4799**	39.1424** 25.7529**	18.5529 11.9034	18299.5550 12446.094	91.021 100.465
Weight of seeds per spike	0.0060 0.0940	0.0995** 0.0942**	0.0843* 0.0586*	0.0455 0.0321	41.2460 30.2060	90.426 104.704
1000-kernel weight	12.2045 35.3210	21.8132** 25.9427**	18.7903** 17.5137**	8.4791 7.8801	8616.7660 8251.1520	90.954 104.127
Yield per plant	16.1310 153.8140	20.8652* 18.2453**	10.3075 8.3171*	15.8876 6.2202	9556.6840 5431.8160	86.462 104.334

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level

** Significant at 1% level

† Corresponding to the missing values in the different characters, the number of degrees of freedom have been subtracted from error D.F. in calculating mean squares.

Plant height was positively correlated with number of spikelets per spike and negatively correlated with weight of seeds per spike and 1000-kernel weight at both locations. It was positively correlated with number of tillers per plant at Ellerslie while at Parkland the correlation coefficient was not significant.

Number of tillers per plant was positively correlated with yield per plant at both locations and with number of spikelets per spike at Ellerslie. Correlation of number of tillers per plant with number of seeds per spike, weight of seeds per spike and 1000-kernel weight was not significant at either location. The correlation coefficients of other components of yield, viz., number of spikelets per spike, number of seeds per spike, weight of seeds per spike and 1000-kernel weight could be explained in the same manner.

As far as yield is concerned, it was highly and positively correlated with 1000-kernel weight, weight of seeds per spike and number of tillers per plant at both locations, but negatively correlated with onset-of-heading and final heading at Ellerslie.

Factor analysis

In the factor analysis, the symmetrical correlation matrix produced for all the characters under study was resolved into a varimax-rotated factor matrix. As suggested by Cattell (1965), if the number of factors is kept equal to that of the variables, 100% of the covariation in the data could be accounted for by these factors. In the present case the data was computerized for five factors which explained 92% of the

TABLE 2

Simple correlation coefficients between ten characters
from F₁ diallel set at two locations.

Character	2	3	4	5	6	7	8	9	10
1. Onset-of-heading	0.916** 0.082	0.196 0.028	0.723** 0.821**	0.145 0.291**	0.313** 0.545**	0.191 0.246**	-0.324** -0.304**	-0.615** -0.612**	-0.281** -0.150
2. Final heading	-	0.548** 0.618**	0.744** 0.790**	0.196 0.358**	0.257** 0.588**	0.150 0.267*	-0.331** -0.240*	-0.574** -0.547**	-0.278** -0.058
3. Heading-span		-	0.316** 0.241*	0.166 0.219	-0.022 0.270*	-0.012 0.122	-0.135 -0.006	-0.146 -0.114	-0.147 0.105
4. Plant height			-	0.365** 0.239	0.416** 0.601**	0.149 0.106	-0.250* -0.402**	-0.474** -0.612**	-0.026 -0.162
5. Number of tillers per plant				-	0.272* 0.194	-0.014 0.085	0.059 -0.039	0.117 -0.121	0.574** 0.320**
6. Number of spikelets per spike					-	0.582** 0.556**	0.280* 0.206	-0.225 -0.207	0.154 0.184
7. Number of seeds per spike						-	0.663** 0.659**	-0.165 -0.014	0.144 0.211
8. Weight of seeds per spike							-	0.624** 0.740**	0.502** 0.506**
9. 1000-kernel weight								-	0.512** 0.500**
10. Yield per plant									-

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level

** Significant at 1% level

total variability with respect to all the characters at respective locations. The values of the rotated factor matrix in terms of the factor loadings together with the communalities for ten characters are given in Table 3.

The first factor was termed *lateness* because it carried the highest loadings for onset-of-heading and final heading at both locations and explained 28% and 32% of the variation in the data at Ellerslie and Parkland. Yield per plant was negatively affected by this factor showing thus that higher the number of days taken by a particular entry to head the larger will be its contribution to *lateness* and lower will be its yield and 1000-kernel weight. Plant height was one of the major contributors to *lateness* as it carried high loadings at both locations. This corresponds proportionally to the positive association between days to head and height of the plant. Number of tillers per plant, number of spikelets per spike and number of seeds per spike contributed very little to this factor.

The second principal factor was termed *yielding ability* as it carried generally higher loadings for yield and yield components: spikelets per spike, number of seeds per spike and, (except at Ellerslie) 1000-kernel weight at both locations. This factor accounted for about 19% of the variation. The loadings on yield and its components for this factor, as against those of the first factor (*lateness*), support a negative relationship between *lateness* and *yielding ability*. There is very little contribution of plant height and number of tillers per plant for this factor at either location.

TABLE 3

Varimax rotated factor matrix for ten characters
from F₁ diallel set at two locations

Character	Communalities	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5
Onset-of-heading	0.964 0.908	0.960 0.892	0.107 -0.242	-0.060 0.062	-0.167 -0.093	-0.010 0.205
Final heading	0.972 0.945	0.901 0.773	0.070 -0.173	-0.022 0.073	-0.153 0.516	0.363 0.212
Heading-span	0.994 1.000	0.215 0.123	-0.040 0.032	0.033 0.039	-0.032 0.987	0.972 0.086
Plant height	0.806 0.906	0.788 0.917	0.175 -0.174	0.294 -0.113	-0.224 0.132	0.139 0.066
Number of tillers per plant	0.886 0.961	0.182 0.177	0.038 0.126	0.915 0.807	-0.010 0.113	0.121 0.949
Number of spikelets per spike	0.867 0.824	0.188 0.756	0.847 0.199	0.282 0.431	-0.182 0.160	-0.047 -0.039
Number of seeds per spike	0.923 0.971	0.160 0.218	0.882 0.626	-0.133 0.957	0.321 0.050	0.005 0.061
Weight of seeds per spike	0.990 0.963	-0.249 -0.258	0.523 0.567	0.086 0.754	0.804 -0.012	-0.034 -0.088
1000-kernel weight	0.884 0.878	-0.486 -0.518	-0.227 0.747	0.268 0.143	0.724 -0.060	-0.030 -0.169
Yield per plant	0.851 0.863	-0.170 0.011	0.109 0.876	0.762 0.114	0.456 0.043	-0.145 0.282
Percent of total variability explained	91.396 92.187	28.203 32.355	18.808 18.226	16.589 17.273	16.165 13.131	11.361 11.202

First reading under each column refers to Ellerslie and the second to Parkland.

The term *tillering-capacity* was chosen for the third principal factor, as the number of tillers per plant contributed highest at both locations. The factor explains approximately 17% of the total variation and is supported by number of spikelets per spike, number of seeds per spike (at Parkland), weight of seeds per spike, 1000-kernel weight and yield per plant. Since this component is closely associated with the *yielding-ability*, the *lateness* factor shows negative effects for onset-of-heading and final heading. This kind of response seems to be logical since high tillering capacity results in higher yield per plant and is associated with earliness.

The fourth principal component, named *heading-period* at Parkland and *seed weight* at Ellerslie, accounted for 13% and 16% of the variation respectively. Different names were chosen for different locations because of the inconsistency between locations of factor loadings on various characters. At Ellerslie, the *seed-weight* component was affected by number of seeds per spike, 1000-kernel weight and yield per plant. The contribution of onset-of-heading, final heading, heading-span, plant height and number of tillers per plant towards this component was negative. At Parkland, *heading-period* was positively affected by final heading, plant height, number of tillers per plant and number of spikelets per spike.

The terms *heading-period* and *tillering-capacity* were also used for fifth principal component at Ellerslie and Parkland, respectively, because of their high contribution towards the loadings of this factor. Only 11% of the total variability was accounted for by this factor at both

TABLE 4

Estimates of general combining ability
of five parental lines used in F₁ diallel set
for ten characters at two locations

Character	Marquis	Chinook	Khush-hal	Ciano	Inia
Onset-of-heading	1.933 1.9867	1.4667 2.3533	-0.4666 -0.8800	-1.7334 -2.2466	-1.2000 -1.2133
Final heading	2.1600 2.4800	1.7934 2.9466	-0.3733 -1.0867	-2.1066 -2.4867	-1.4733 -1.8533
Heading-span	0.2600 0.4800	0.3933 0.5800	0.1267 -0.2200	-0.4400 -0.2200	-0.3400 -0.6200
Plant height	13.7470 12.3968	12.1740 13.4648	-8.1473 -8.7599	-7.8220 -7.9252	-9.9516 -9.1766
Number of tiller per plant	-0.0409 0.3351	0.8629 0.3316	0.6390 0.5466	-0.3116 -0.1349	-1.1495 -1.0784
Number of spikelets per spike	0.5123 0.6729	0.3536 0.4595	-0.5752 -0.5058	-0.3151 -0.3616	0.0245 -0.2650
Number of seeds per spike	2.8305 2.0515	-1.5451 -0.9495	-1.1460 0.3450	-1.9094 -2.4385	1.7700 0.9916
Weight of seeds per spike	-0.0103 -0.0326	-0.1285 -0.0958	-0.0092 0.0848	0.0008 -0.0501	0.1472 0.0938
1000-kernel weight	-2.4230 -2.3256	-1.5338 -1.3217	0.7291 1.6523	1.7007 0.8898	1.5269 1.1052
Yield per plant	-0.1646 -0.4672	-1.2333 -0.5154	-0.0382 0.3461	0.1903 0.2629	1.2458 0.3736

First reading under each column refers to Ellerslie and the second to Parkland.

locations. The factor was negatively affected by number of spikelets per spike, weight of seeds per spike and 1000-kernel weight.

Combining ability analysis

Estimates of general and specific combining ability for the F_1 diallel were obtained by Griffing's (1956) procedure following method 1, model 1. General combining ability (GCA) values for all the characters at both locations are given in Table 4. Marquis appeared to be the best combiner for onset-of-heading, final heading, plant height, number of spikelets per spike and number of seeds per spike at both locations. For tillering capacity Chinook exhibited the highest combining ability at Ellerslie while Khush-hal excelled Chinook at Parkland. Inia showed the highest general combining ability for yield per plant, 1000-kernel weight and weight of seeds per spike at both locations. It is interesting to note that Inia excelled Marquis and Chinook (both Canadian standard varieties) in general combining ability for yield in a foreign environment. This might be attributed to a better adaptability of Inia as compared to the other two introductions, viz., Khush-hal and Ciano, of Pakistan and Mexican origin. Generally it could be said that Canadian environments are less suitable for introductions like Khush-hal and Ciano as far as yield per plant is concerned.

The values of specific combining ability (SCA), reciprocal effects and variances for general and specific combining abilities for F_1 hybrids are given in Tables 5 to 15.

Cross (CxI) had the highest SCA for onset-of-heading (Table 5),

Estimates of specific combining ability, reciprocal effects and variances
of general and specific combining ability from F_1 diallel set at two locations.

TABLE 5. Onset-of-heading

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia		
Marquis	-	0.8667 0.6801	-0.5333 -0.0866	-1.1000 -0.8866	-1.2999 -1.2533	1.9333 1.9867	-0.2104 -0.5095
Chinook	-0.3333 0.1667	-	-0.9000 0.3800	-0.4667 0.2467	-0.5000 -1.1200	1.4667 2.3533	0.0400 -0.3554
Khush-hal	0.0 -0.1667	-0.5000 0.0	-	0.1333 -0.6867	0.4333 -0.8867	-0.4666 -0.8800	0.1544 -0.4589
Ciano	-0.5000 -2.0000**	0.0 -0.1667	0.6667 0.0	-	1.0334 0.9800	-1.7334 -2.2466	0.2715 -0.0701
Inia	0.5000 1.0000	0.5000 0.1667	0.8333* -0.5000	-0.1667 1.0000	-	-1.2000 -1.2133	0.8548 1.0144

Reciprocal effects

TABLE 6. Final heading

Marquis	-	1.0733 2.9200	-0.9267 -1.7133	-1.3600 -1.4799	-1.6000 -1.4467	2.1600 2.4800	-0.2335 -0.6322
Chinook	0.0 0.0	-	-0.8934 -1.6799	-0.3267 -1.2800	-0.2933 -2.0800	1.7934 2.9466	0.1505 2.2100
Khush-hal	-0.5000 0.3333	-0.5000 -0.1667	-	-0.4933 0.2534	-0.1266 0.6200	-0.3733 -1.0867	0.3187 1.2870
Ciano	-0.3333 -1.1667	0.0 -1.1667	0.0 0.0	-	0.9400 1.1867	-2.1066 -2.4867	0.4979 0.6653
Inia	0.8333 0.1667	0.0 0.0	0.0 0.0	0.0 -0.1667	-	-1.4733 -1.8533	0.5436 2.1050

Reciprocal effects

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level

** Significant at 1% level

at both locations followed by hybrid (MxCH). This shows that hybrid (CxI) was latest in heading and implicitly in maturity. Cross (MxI) exhibited lowest SCA and hence could be regarded as the earliest of all the F_1 's. It is interesting to note that for both locations, the best hybrid, with the highest SCA, had parents showing the lowest GCA's, while the poorest hybrid, with the lowest SCA, had the female parent with the highest GCA and the male parent with the lowest GCA. Thus it appears unlikely that the best performing parents (those with high GCA's) necessarily produce hybrids showing high SCA's. None of the hybrids showed significant reciprocal effects except (IxK) at Ellerslie and (CxM) at Parkland, and the parental variances for GCA were in general higher than for SCA.

With respect to final heading (Table 6) and heading-span (Table 7), although there are some differences in relative positions of the parents and hybrids concerned, the general conclusions are the same as for onset-of-heading.

With respect to highest SCA for plant height (Table 8) at both locations, the best hybrid was (MxCH) and the poorest (MxI). The parents of cross (MxCH) had the highest GCA at both locations while the poorest hybrid had Marquis as one parent, with the highest GCA and Inia as the other, with the lowest GCA. The parental GCA-variances were larger than their SCA-variances at both locations, suggesting a greater importance of additive gene effects for the parental lines than of non-additive ones for the hybrids, with respect to plant height. The reciprocal effects were significant for (CxM) at both locations and for (IxM) and (IxCH) at Ellerslie. In the case of (IxM), the reciprocal effects could be attributed

Estimates of specific combining ability, reciprocal effects and variances
of general and specific combining ability from F₁ diallel set at two locations.

TABLE 7. Heading-span

♀ Parent	Specific combining ability					GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis	-	2.2533 0.0400	-1.6133 -0.0267	-0.6133 -0.2933	-0.2133 0.1067	0.4800 0.2600	-0.0163 -0.1184	-0.2096 -0.8721
Chinook	-0.1667 0.3333	-	-2.0467 -0.1600	-1.5467 0.0733	-0.9800 0.1400	0.5800 0.3933	0.0709 -0.0124	-0.2091 0.8204
Khush-hal	0.5000 0.0	-0.1667 0.0	-	0.9200 -0.6600	1.4867 -0.5933	-0.2200 0.1267	-0.0678 -0.3004	-0.2009 1.3018
Ciano	0.8333* 0.1667	0.0 0.0	0.0 -0.6667	-	0.3200 -0.0267	-0.2200 -0.4400	0.1097 -0.3004	-0.0340 -0.3328
Inia	-0.8333* 0.3333	-0.1667 -0.5000	0.5000 -0.8333	-1.3333** 0.1667	-	-0.6200 -0.3400	0.0317 0.0356	-0.0817 0.2341

Reciprocal effects

TABLE 8. Plant height

Marquis	-	3.4117 3.6766	2.0390 2.7912	-2.3879 -1.9234	-4.1867 -4.4220	13.7470 12.3968	187.1822 151.7148	-4.4931 -4.9129
Chinook	0.2933 -0.1134	-	2.4237 1.5132	1.3784 3.0219	2.6996 -3.3567	12.1740 13.4648	146.4086 179.3356	-0.5994 -0.4071
Khush-hal	-0.4766 1.2467	0.8250 1.8566	-	-1.9553 -0.1367	-0.0704 -0.0287	-8.1473 -8.7599	64.5814 74.7702	-1.1491 -1.5526
Ciano	-3.7717* -4.3133	-1.3083 -0.7933	0.9233 1.3100	-	1.3890 2.0900	-7.8220 -7.9252	59.3868 60.8436	-0.6846 -0.6295
Inia	5.1567** 3.3467	-4.5567* -1.4767	1.0980 2.1400	-2.0700 -0.5600	-	-9.9516 -9.1766	97.2374 82.2441	4.4238 6.8172

Reciprocal effects

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level

**Significant at 1% level

Estimates of specific combining ability, reciprocal effects and variances
of general and specific combining ability from F_1 diallel set at two locations.

TABLE 9. Number of tillers per plant

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia		
Marquis	-	-0.0903 -0.8068	-0.7628 -1.2051	0.5342 -0.3143	-0.1946 -1.1968	-0.0409 0.3351	-0.8224 -0.7787
Chinook	1.1667 0.0667	-	1.8354 0.5318	-0.1528 -0.5535	-0.4983 -0.3683	0.8629 0.3316	-0.8197 -0.5617
Khush-hal	-0.4297 1.0167	0.1055 -0.6833	-	-0.3790 0.5982	-0.3183 -0.0249	0.0794 -0.0127	0.4944 -0.2004
Ciano	0.4833 0.1593	-0.5000 -1.1167	0.7833 0.6167	-	0.5094 1.0399	-0.2319 -0.2933	-0.6716 -0.5244
Inia	-0.4500 0.6000	-1.2500 0.4083	0.8227 0.4167	0.3500 -0.7333	-	0.9923 0.8513	-0.6077 0.1064

Reciprocal effects

TABLE 10. Number of spikelets per spike

Marquis	-	-0.2740 1.1008	0.1741 -0.2395	-0.0388 -0.1238	-0.4728 -0.1136	0.5123 0.6729	-0.3687 -0.2192
Chinook	-0.3333 0.2668	-	0.2618 0.1404	0.3642 -0.1925	-0.0032 -0.5073	0.3536 0.4595	-0.3436 0.1847
Khush-hal	1.0593 -0.3278	-0.2623 -0.3167	-	-0.3403 0.1615	-0.1155 -0.3017	-0.5752 -0.5058	-0.3357 -0.1935
Ciano	-0.0778 -0.4012	-0.1002 -0.0277	0.4888 0.2057	-	0.2157 0.5208	-0.0482 0.0431	-0.2854 -0.1931
Inia	-0.4388 -0.2390	0.1947 0.3458	0.4692 0.1447	0.0222 -0.2168	-	0.0245 -0.2650	-0.2742 -0.0073

Reciprocal effects

First reading under each column refers to Ellerslie and the second to Parkland.

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F₁ diallel set at two locations.

TABLE 11. Number of seeds per spike

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia		
Marquis	-	-1.9659 1.2486	2.2792 0.1486	0.9872 -1.2352	-3.1363 1.7185	2.8305 2.0515	-3.5029 -2.7300
Chinook	-0.6665 0.1168	-	0.0151 0.1107	0.9075 -0.3172	2.0447 0.1696	-1.5451 -0.9495	-2.2146 -2.2104
Khush-hal	3.1140 1.5667	-1.3513 -0.7168	-	-2.5752 -0.1725	-0.3525 -2.4527	-1.1460 0.3450	-1.7712 -2.2186
Ciano	4.5557** 0.4772	1.7223 0.5945	-0.6055 1.0333	-	2.9756 1.9031	-1.9094 -2.4385	-0.6930 -2.1780
Inia	-1.5222 -1.1278	0.0723 1.5223	-0.7965 -0.8835	-2.2833 -1.1335	-	1.7700 0.9916	4.1624 1.4764

Reciprocal effects

TABLE 12. Weight of seeds per spike

Marquis	-	-0.0905 0.0512	0.0739 -0.0038	0.1517 0.0746	-0.1100 0.0983	-0.0103 -0.0326	-0.0083 -0.0095
Chinook	-0.0175 -0.0320	-	0.0364 0.0194	0.0412 -0.0762	0.0439 0.0399	-0.1285 -0.0958	-0.0056 -0.0087
Khush-hal	0.1782* -0.0287	-0.0788 -0.0527	-	-0.1029 0.0249	0.0727 -0.0356	-0.0092 0.0846	-0.0061 -0.0094
Ciano	0.2843** 0.0622	0.0267 0.0268	-0.0705 0.1142	-	0.0391 0.0487	0.0008 -0.0501	0.0036 -0.0055
Inia	-0.0590 -0.0805	-0.1433 -0.0038	0.0425 0.0427	-0.0505 -0.0460	-	0.1472 0.0938	-0.0014 -0.0046

Reciprocal effects

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level

** Significant at 1% level

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F_1 diallel set at two locations.

TABLE 13. 1000-kernel weight

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano			
Marquis	-	-0.1201 0.0835	-0.5650 -0.2523	2.0236 2.6151	0.1734 0.8063	-2.4230 -2.3256	-2.6455 -1.2556
Chinook	0.2312 -0.7130	-	0.7965 0.3194	0.0375 -1.5360	-0.7600 0.9759	-1.5338 -1.3217	-2.5316 -1.2425
Khush-hal	1.1725 -1.7405	-0.6182 -0.4882	-	0.0280 0.7257	1.8405 1.4420	0.7291 1.6523	-1.1211 -1.2450
Ciano	2.1175 1.0338	-0.9577 0.1613	-1.2283 1.7450	-	-1.5895 -0.4875	1.7007 0.8898	-0.6646 -0.9974
Inia	-0.0403 -1.0033	-3.1908* -1.3335	1.4478 1.8997	0.8910 0.0420	-	1.5269 1.1052	-1.2788 -0.9555

TABLE 14. Yield per plant

Marquis	-	-0.5845 -0.1980	-0.9024 0.1755	2.4220 0.8520	-0.3343 0.0911	-0.1646 -0.4672	-1.0311 -0.2840	-2.6455 -1.2556
Chinook	1.1575 -0.6980	-	1.9387 0.0337	0.0545 -0.2106	-0.7460 -0.6938	-1.2330 -0.5154	0.4628 -0.2366	-2.5316 -1.2425
Khush-hal	0.3260 -0.1923	-0.7188 -0.5447	-	-0.2716 -0.0804	1.6500 0.2976	-0.0382 0.3461	-1.0567 -0.3825	-1.1211 -1.2450
Ciano	2.5833 -2.0633*	-0.5388 -0.3382	0.8368 1.6012	-	-0.9329 0.5674	0.1903 0.2629	-1.0220 -0.4331	-0.6646 -0.9974
Inia	-0.2452 -1.0785	-3.2108* -0.0700	0.5890 2.5692*	0.5675 -0.4895	-	1.2458 0.3736	0.4939 -0.3626	-1.2788 -0.9555

First reading under each column refers to Eilerslie and the second to Parkland.

*Significant at 5% level

to the female parent (Inia) while for (CxM) and (IxCH), the male parents Marquis and Chinook are responsible, because of the negative sign associated with the effects.

For number of tillers per plant (Table 9), the hybrids (CHxK) and (CxI) had the highest SCA's at Ellerslie and Parkland respectively. The parental GCA for (CHxK) at Ellerslie was highest whereas that for (CxI) at Parkland was the lowest. The poorest hybrid was (MxK) at both locations, having the lowest SCA value, although one of its parents (Khush-hal) showed high GCA. The variances for GCA were generally higher than those for SCA.

Hybrid (CHxC) at Ellerslie and (MxCH) at Parkland, respectively ranked highest for number of spikelets per spike with respect to their SCA's, whereas cross (MxI) at Ellerslie and (CxI) at Parkland ranked lowest. It could be argued that the hybrid (MxI) had one parent (Marquis) ranking highest in GCA and hybrid (CHxC) had one parent (Ciano) with a very low GCA which shows that high parental GCA's might not result in higher SCA's for the hybrids. In general, the variances for GCA, were higher than those for SCA. The reciprocal effects were non-significant for all crosses.

The interpretation of the results for general and specific combining ability and the reciprocal effects for number of seeds per spike (Table 11), weight of seeds per spike (Table 12), 1000-kernel weight (Table 13) and yield per plant (Table 14) follow the same pattern. Differences may be found with respect to relative positions of the parents and hybrids concerned but the general conclusions are the same.

TABLE 15

Analysis of variance of general and specific combining ability
for ten characters from F_1 diallel set at two locations.

Character	M.S. for GCA	M.S. for SCA	M.S. for reciprocal effects	Error M.S.
D.F.	4	10	10	48
Onset-of-heading	26.3438** 41.9375**	1.9125** 2.2312**	0.4556 1.2722	0.3155 0.7640
Final heading	36.5000** 64.0469**	2.8562** 7.1312**	0.2611 0.3167	0.3504 0.9482
Heading-span	1.3688** 2.6199	0.4951 4.5816**	0.3333 0.7500	0.3144 1.3089
Plant height	1409.4062** 1396.7344**	22.8000** 22.6250**	14.1257* 8.6772	6.7393 7.3723
Number of tillers per plant	6.4326** 4.2588*	1.2214 2.6332*	1.0437 0.8791	1.2336 1.1674
Number of spikelets per spike	2.0459* 2.8027**	0.2086 0.5035	0.4016 0.1455	0.5531 0.3284
Number of seeds per spike	46.2188** 30.4062**	9.3219 4.4004	8.8449 2.0571	5.2554 4.0978
Weight of seeds per spike	0.0959** 0.0719**	0.0169 0.0137	0.0306* 0.0065	0.0124 0.0142
1000-kernel weight	34.9531** 29.7500**	3.0262 5.2500	4.3586 2.8623	3.2919 2.7816
Yield per plant	7.8486 2.0332	3.8074 0.6977	4.1329 3.1529	3.9663 1.8834

First reading under each column refers to Ellerslie and the second to parkland.

* Significant at 5% level

**Significant at 1% level

A general review of the results of the combining ability analyses with respect to all the characters under study suggests that:

(i) The high GCA of the parents can not be taken as a criterion for the evolution of hybrids with high SCA's since the hybrids with high SCA's were associated with respective parents of low GCA's and *vice versa*.

(ii) Since the variances for GCA were usually larger than those for SCA, and since GCA is the result of additive, and SCA non-additive gene effects (Sprague and Tatum, 1942; Fryxel *et al* 1958 and Griffing 1956), the selection of the parental lines on the basis of their GCA's should be given priority over selection on the basis of their SCA's. This conclusion may also be supported from the analysis of variance for general and specific combining ability (Table 15). The results of Table 15 reveal that the variances for GCA were significant except for heading-span at Parkland and for yield per plant at both locations. The variances for SCA were significant only for onset-of-heading, final-heading and plant height (at both locations) and for heading-span and number of tillers per plant (at Parkland). Significance of variances for GCA thus suggests the importance of additive gene effects and emphasizes that substantial differences exist among the parental lines used in the study. (iii) The significant variances for SCA imply that non-additive gene effects for the particular characters are relatively more important and that the hybrids with highest SCA's may be selected for further breeding adaptability tests.

TABLE 16

Mean squares from the analysis of variance
of the $5 \times 5 F_1$ diallel table for ten characters at two locations.

Source of variation	D.F.	Onset-of-heading	Final heading	Heading-span	Plant height	Number of tillers per plant	Number of spikelets per spike	Number of seeds per spike	Weight of seeds per spike	1000 kernel weight	Yield per plant
<i>a</i>	4	79.1719** 125.8750**	109.6875** 192.2500**	4.1074 7.8604	4228.0000** 4191.0000**	19.3008* 12.7686	6.1328* 8.4102**	138.7031* 91.2188	0.2877* 0.2156*	104.8281* 89.2031**	23.5332 6.0947
<i>b</i>	10	5.7750 6.7125*	8.5250** 21.3812**	1.4852 13.7445*	68.4000 67.7000	3.6668 7.9043	0.6289 1.5145	28.0187 13.2562	0.0507 0.0413	9.0875 15.7437	11.4297 2.1000
<i>b</i> ₁	1	16.3333 20.8033	38.1633 66.2700	5.8800 12.4033	67.5947 31.1918	0.7123 15.8674	0.1574 0.5796	4.1706 3.7705	0.0726 0.1749	10.4398* 66.0398	15.1135 2.0817
<i>b</i> ₂	4	2.4219 4.7959	4.4375* 1.0469	1.8822 5.1289	112.5625 93.1719*	2.4049 13.1418*	0.7930 1.1104	14.0703 14.2686	0.0092 0.0390	5.3457 8.9922	5.1953 3.6924
<i>b</i> ₃	5	6.3625** 5.4500*	5.8500** 28.6750**	0.2883 20.1060*	33.0125 54.8625**	5.2719 2.1195	0.5953 2.0281	43.9750 14.3625*	0.0796 0.0166	11.8000 11.1000	15.6836 0.8312
<i>c</i>	4	2.1333 4.1833	0.6167 0.5833	1.4333 2.4667	11.1538 6.6066	3.8020 1.9934	0.0725 0.4659	37.5303 4.8971	0.0977 0.0398	11.6772 14.9461	18.0605 12.4107
<i>d</i>	6	0.8556 3.5722*	0.8944 1.1944	0.7111 2.1056	63.1929* 38.9815**	2.6837 3.0668	1.9599 0.4170	19.2044 7.0210	0.0880* 0.0061	14.0084 4.3472	8.6244 7.4908
Blocks $\times a$	8	1.0312 3.5937	0.6328 4.6406	2.2113 5.6348	17.7266 35.6094	4.7915 4.7622	1.7173 0.8608	25.6719 24.4531	0.0542 0.0572	20.7422 7.6406	7.8745 5.7969
Blocks $\times b$	20	1.1312 2.5469	0.6406 3.6719	0.7294 5.1647	27.3656 24.7844	4.9238 4.9705	2.1734 0.9705	19.0937 6.5250	0.0398 0.0412	8.8656 10.3906	15.2057 5.3535
Blocks $\times b_1$	2	9.2467 8.8466	2.4866 15.8600	1.5800 6.2067	77.0164 270.1160	13.4714 38.0653	2.2294 0.0713	42.1510 6.3986	0.0717 0.1328	0.4583 33.9540	47.2437 1.2041
Blocks $\times b_2$	8	1.0688 4.0024	0.9307 1.3726	1.0355 6.2955	31.9712 20.4922	4.3863 1.9459	1.3899 1.5215	16.3374 10.4585	0.0487 0.0377	8.8271 8.2334	8.9218 3.0371
Blocks $\times b_3$	10	0.4750 0.9937	0.3000 4.6562	0.4725 4.6720	21.6625 6.1187	4.9898 2.8008	3.0066 0.7113	20.9125 4.0633	0.0335 0.0390	10.6437 10.8035	18.5426 8.1539
Blocks $\times c$	8	0.8333 2.1833	1.4667 0.4083	1.0583 2.1417	16.0278 24.9243	3.1607 3.1579	1.2033 1.3036	12.4407 17.3466	0.0273 0.0666	6.5340 7.7739	8.6371 8.0467
Blocks $\times d$	12	0.6389 1.0722	1.7444 1.8944	0.3778 1.9056	13.0140 6.9826	1.3007 1.9370	1.0707 0.8900	5.8792 10.4261	0.0293 0.0204	6.5789 5.8304	11.2731 4.4533
Error	48	0.9418 2.2921	1.0529 2.8450	0.9433 3.9244	20.2814 22.1612	3.7021 3.5057	1.6601 0.9876	15.7776 12.2919	0.0375 0.0429	9.8848 8.354	11.9059 5.6517

*Significant at 5% level

** Significant at 1% level

First reading under each column refers to Ellerslie and second to Parkland. Error D.F. comprises of block interaction with D.F. of $(a+b+c+d)$. Each component has been tested against its own block interaction.

Diallel cross analysis

F_1 entries from Appendices III to XXII were sorted out and complete diallel tables were constructed for each replication with respect to all the characters at both locations. All the entries were subjected to Hayman's (1954a) analysis of variance. The results of this analysis are presented in Table 16. In this table component a tests the significance of additive effects and b the dominance effects of genes, while b_1 tests the mean deviations of F_1 's from their mid-parent values. The dominance-deviations, if predominantly in one direction, may result in significance of b_1 in an analysis of variance. The component b_2 indicates the extent to which the mean dominance deviations within a given array of the diallel table differ from those of the other arrays. A significant b_2 thus implies that some of the parents contain an excess of dominant alleles. The b_3 component tests the portion of the dominance deviations attributable to individual F_1 's. The difference between the reciprocal crosses is assessed by the significance of the c component and maternal effects not ascribable to c are reflected by d . In Table 16 each of the components has been tested for significance against its own block-interaction mean-square. The c was not significantly different from zero at either location for any of the characters studied. Substantial differences among the parents are suggested by the significance of the a component (additive gene effects) for onset-of-heading, final heading, plant height, number of spikelets per spike and 1000-kernel weight at both locations and number of tillers per plant and number of seeds per spike at Ellerslie). Item b was significant for final heading at both locations and for onset-of-heading and heading-span at Parkland.

TABLE 17

Analysis of variance of $W_p - V_p$ differences
for ten characters from F_1 diallel set at two locations.

Character	Block M.S.	Entry M.S.	Error M.S.	F for Entries
Onset-of-heading	9.2560 18.9050	0.5815 0.0396	0.1617 0.2974	3.4689 0.1332
Final heading	5.1354 73.2777	1.4540 11.9745	0.4502 4.6422	3.2297 2.5795
Heading-span	0.9138 31.5321	0.1887 18.5786	0.1845 11.9478	1.0227 1.5550
Plant height	17021.1562 4453.5938	344.3281 180.5625	200.6953 58.2656	1.7157 3.0990
Number of tillers per plant	37.6399 9.8287	6.5010 0.7379	3.5646 2.0809	1.8238 0.3546
Number of spikelets per spike	4.3689 0.5617	0.7859 0.1118	0.2638 0.1160	2.9796 0.9640
Number of seeds per spike	989.3882 24.4063	83.1030 23.2917	64.5087 12.2852	1.2882 1.8959
Weight of seeds per spike	0.0021 0.0041	0.0002 0.0002	0.0003 0.0002	0.5844 1.1813
1000-kernel weight	128.4015 134.1506	7.3713 21.2359	6.6094 7.2551	1.1153 2.9270
Yield per plant	102.4395 28.0996	13.8542 5.8340	11.9046 5.6502	1.1638 1.0325

First reading under each column refers to Ellerslie and the second to Parkland.

Directional dominance (significance of b_1) was exhibited by 1000-kernel weight at Ellerslie. Significance of b_2 for final heading at Ellerslie and for plant height and number of tillers per plant at Parkland indicates that some parents probably possess more dominant alleles than others for these characters.

The assumptions of no non-allelic interaction, no multiple allelism and uncorrelated parental gene distribution, were checked by analysis of the variance of $W_r - V_r$. The test of homogeneity of $W_r - V_r$ is given in Table 17. None of the characters showed heterogeneity at either location and the conditions underlying the diallel cross analysis could therefore be accepted as valid. For analysis of the genetic components of variation, the offdiagonal values of the diallel table were replaced with the common mean of the corresponding cross and its reciprocal. The array variances (V_r) and parent-offspring covariances (W_r) over five arrays provided the basis for calculating other second degree statistics which are presented in Table 18. The estimates of genetic components of variation obtained from second degree statistics (Hayman 1954b) are presented in Table 19. Table 18 supplied 35 statistics [(15 V_r 's of five arrays and three replications, 15 W_r 's, V_{OLO} , W_{OLO1} , V_{OL1} , V_{1L1} and $(M_{L1} - M_{LO})^2$] and 10 constants were fitted to them (5 F_r values, D , H_1 , H_2 , h and E ; F was not considered, as it is the mean of five F_r 's), leaving 25 degrees of freedom for error to test the significance of genetic components of variation. The proportional estimates of the genetic parameters from Table 19 for all the characters are given in Table 20. The results shown in Table 19 and 20 supported by the

TABLE 18

Estimates of second degree statistics parameters
for ten characters from F_1 diallel set at two locations.

Character	V_{OLO}	W_{OLO1}	V_{OL1}	V_{1L1}	$[M_{L1} - M_{LO}]^2$
Onset-of-heading	15.0000 15.7002	6.2693 7.8816	2.6367 4.1963	3.6055 5.3152	0.8710 1.1096
Final heading	16.9668 27.1514	7.6781 13.1479	3.6621 6.4092	5.0816 9.9770	2.0354 3.5344
Heading-span	0.5889 3.6111	0.1901 0.8584	0.1370 0.2621	0.3845 2.5528	0.3136 0.6614
Plant height	486.7744 518.4434	257.0203 264.6565	140.9746 139.7002	152.3508 150.9949	3.6043 1.6638
Number of tillers per plant	1.4343 5.4749	0.8816 1.1369	0.6432 0.4255	1.2544 1.7429	0.0379 0.8462
Number of spikelets per spike	1.2283 0.5749	0.4720 0.3638	0.2047 0.2805	0.3093 0.5328	0.0083 0.0309
Number of seeds per spike	28.9980 12.2275	11.1666 5.3820	4.6221 3.0371	9.2889 5.2459	0.2224 0.2010
Weight of seeds per spike	0.0384 0.0360	0.0187 0.0142	0.0096 0.0072	0.0180 0.0141	0.0038 0.0093
1000-kernel weight	16.7744 13.1670	7.4203 5.8156	3.4941 2.9736	5.0057 5.5967	0.5568 3.5220
Yield per plant	5.4558 0.8875	1.8886 0.2405	0.7846 0.2034	2.6896 0.5532	0.8060 0.1110

First reading under each column refers to Eilerslie and the second to Parkland.

TABLE 19

Estimates of components of variation
for ten characters from F_1 diallel set at two locations.

Character	D	F	H_1	H_2	h^2	E
Onset-of-heading	14.6845 ± 0.3196** 14.9359 ± 0.4053**	4.5440 ± 0.7983** -1.0433 ± 1.0125	3.5241 ± 0.8630** 3.4473 ± 1.0946**	3.2439 ± 0.7828** 2.9471 ± 0.9924**	3.2826 ± 0.5285** 3.9492 ± 0.6703**	0.3155 ± 0.1305 0.7643 ± 0.165**
Final heading	16.6165 ± 0.5209** 26.2030 ± 1.0947**	2.8008 ± 1.3011* 0.5733 ± 2.7346	5.6702 ± 1.4066** 12.0021 ± 2.9564**	4.9776 ± 1.2758** 12.3744 ± 2.6815**	7.9178 ± 0.8614** 13.5304 ± 1.8104**	0.3503 ± 0.2126 0.9484 ± 0.4469*
Heading-span	0.2745 ± 0.1321* 2.3939 ± 1.1997*	0.0402 ± 0.3300 2.2189 ± 2.7495	0.5491 ± 0.3568 6.9876 ± 2.9726**	0.3612 ± 0.3236 6.5466 ± 2.6962**	1.0532 ± 0.2185** 1.8088 ± 1.8203	0.3144 ± 0.0539** 1.3018 ± 0.4494**
Plant height	480.0347 ± 4.6656** 511.0740 ± 6.7585**	-62.6197 ± 11.6546** -30.5825 ± 16.8827	50.5735 ± 12.5999** 44.6366 ± 18.2521*	32.0255 ± 11.4283** 30.4400 ± 16.5549	10.1059 ± 7.7158 1.9389 ± 11.1770	6.7396 ± 1.9047** 7.3694 ± 2.7591**
Number of tillers per plant	0.2006 ± 0.5712 4.3068 ± 0.3862**	-2.1383 ± 1.4269 5.005 ± 0.9648**	-0.2819 ± 1.5427 4.8621 ± 1.0430**	-0.0226 ± 1.3992 2.9335 ± 0.9460**	-0.6376 ± 0.9447 2.6375 ± 0.6387**	1.2336 ± 0.2332** 1.1618 ± 0.1577**
Number of spikelets per spike	0.6753 ± 0.0312** 0.2460 ± 0.2050	-0.0951 ± 0.0780 -0.7193 ± 0.5121	-0.8602 ± 0.0844** 0.3765 ± 0.5536	-0.6873 ± 0.0765** 0.3513 ± 0.5021	-0.3203 ± 0.0517** -0.0868 ± 0.3399	0.5530 ± 0.0128** 0.3289 ± 0.0837**
Number of seeds per spike	23.7437 ± 2.5748** 8.1325 ± 1.5171**	7.0245 ± 6.4318 -1.9871 ± 3.7897	7.8258 ± 6.9535 1.0359 ± 4.0970	9.1585 ± 6.3069 0.6450 ± 3.7161	-2.4732 ± 4.2581 -1.8166 ± 2.5089	5.2543 ± 1.0511** 4.0951 ± 0.6193
Weight of seeds per spike	0.0259 ± 0.0038** 0.0217 ± 0.0035**	-0.0132 ± 0.0096 -0.0021 ± 0.0086	0.0031 ± 0.0103 -0.0018 ± 0.0093	0.0088 ± 0.0096 -0.0011 ± 0.0085	0.0075 ± 0.0063 0.0282 ± 0.0057**	0.0125 ± 0.0016** 0.0143 ± 0.0014**
1000-kernel weight	13.4832 ± 0.7218** 10.3857 ± 1.0709**	-0.0819 ± 1.8030 -0.2660 ± 2.6750	-1.4414 ± 1.9492 5.0600 ± 2.8920	-0.5364 ± 1.7680 4.9297 ± 2.6231	0.1206 ± 1.1936 12.3080 ± 1.7710**	3.2912 ± 0.2947** 2.7812 ± 0.4372**
Yield per plant	1.4876 ± 0.2376** -0.9960 ± 0.2306**	-1.4048 ± 0.5936* -1.4472 ± 0.5761*	-1.6575 ± 0.6418* -2.7585 ± 0.6229**	-0.3163 ± 0.5821 -2.3675 ± 0.5649**	0.6845 ± 0.3930 -0.7613 ± 0.3814	3.9682 ± 0.0970** 1.8834 ± 0.0942**

First reading under each column refers to Ellerslie and second to Parkland.

* Significant at 5% level

** Significant at 1% level

graphical analysis of regression of W_r upon V_r , lead to the following conclusions:

At both locations, onset-of-heading was inherited as a partially dominant trait, as shown by the mean degree of dominance $[(H_1 \div D)^{1/2} = 0.48]$ and regression line (b_{W_r/V_r}) which passes above the origin (Figure 1). The proportion of genes with positive and negative effects in the parents $[H_2 \div 4H_1]$ is 0.23 at Ellerslie and 0.21 at Parkland, suggesting a slight asymmetry of alleles at the loci exhibiting dominance. The proportion of dominant to recessive genes in the parents $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ is 1.92 at Ellerslie and 0.86 at Parkland, suggesting a preponderance of dominant genes in the parents at Ellerslie and equal proportions of dominant and recessive genes at Parkland. The coefficient of correlation between the parental order of dominance, i.e. $(W_r + V_r)$ and the parental measurements $[(Y_r);$ the corresponding values of the main diagonal of the diallel table] are 0.97 and 0.66 at Ellerslie and Parkland respectively. High positive correlation at both locations suggests an association between recessive genes with late heading and dominant genes contributing towards early heading. This situation is reflected in the standardized deviation graph (Figure 2) where all the Y_r , $(W_r + V_r)$ parental intercepts occupy (+,+) and (-,-) quadrants, except Khush-hal at Parkland. Figure 1 classifies Marquis as the highly recessive and Inia as the highly dominant parents at both locations, since they lie, respectively, farthest and nearest to the point of intersect of regression line and limiting parabola. Figure 2 supplements this conclusion by revealing

TABLE 20

Proportional values of the estimates of genetic parameters for ten characters from F_1 diallel set at two locations.

Character	$[H_1 + D]^{1/2}$	$[H_2 + 4H_1]$	$\left[\frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F} \right]$	h^2/H_2	$r_{Y,W+V}$	Heritability
Onset-of-heading	0.4899* 0.4804*	0.2301* 0.2137*	1.9232* 0.8645*	1.0119* 1.3400*	0.9742 0.6627	0.9837 0.6642
Final heading	0.5842* 0.6768*	0.2195* 0.2578*	1.3372* 1.0329*	1.5907* 1.0934*	0.9712 0.9661	0.7955 0.6325
Heading-span	1.4144 1.7419*	0.1644 0.2342*	1.1093 1.7646 †	2.9160 0.2763	0.1322 0.7382	0.1344 0.1875
Plant height	0.3246* 0.2955*	0.1583* 0.1705*	0.6654* 0.8161†	0.3156 0.0637	0.1720 0.0770	0.7740 0.8299
Number of tillers per plant	1.1855 1.0625*	0.0200 0.1508*	-0.6361 3.4090*	28.1984 0.8991*	0.8341 0.8924	0.0281 0.4885
Number of spikelets per spike	1.1286* 1.2370	0.1997* 0.2333	0.8826† -0.0833	0.4661* -0.2472	-0.2485 0.7543	0.3182 0.0925
Number of seeds per spike	0.5741* 0.3569	0.2606 0.1557	1.6942 0.4900	-0.3031 -2.8162	-0.3653 -0.0519	0.5211 0.2953
Weight of seeds per spike	0.3484 0.2912	0.7000 0.1445	0.1561 0.7188	0.8524 -26.4099	-1.1500 -0.8890	0.2809 0.2739
1000-kernel weight	0.3270 0.6980	0.0930 0.2436	0.9816 0.9640	-0.2248 2.4967	-0.7287 -0.9252	0.5331 0.3869
Yield per plant	1.0556 1.6642	0.0477 0.2146	0.3819 0.3922	-2.1646 0.3216	-0.0082 -0.8646	0.0869 -0.1905

First reading under each column refers to Ellerslie and second to Parkland.

*Genetic component of variation for characters significantly different from zero at $P \leq 0.05$.

†Components D and H_1 significant, F non-significant ($P > 0.05$).

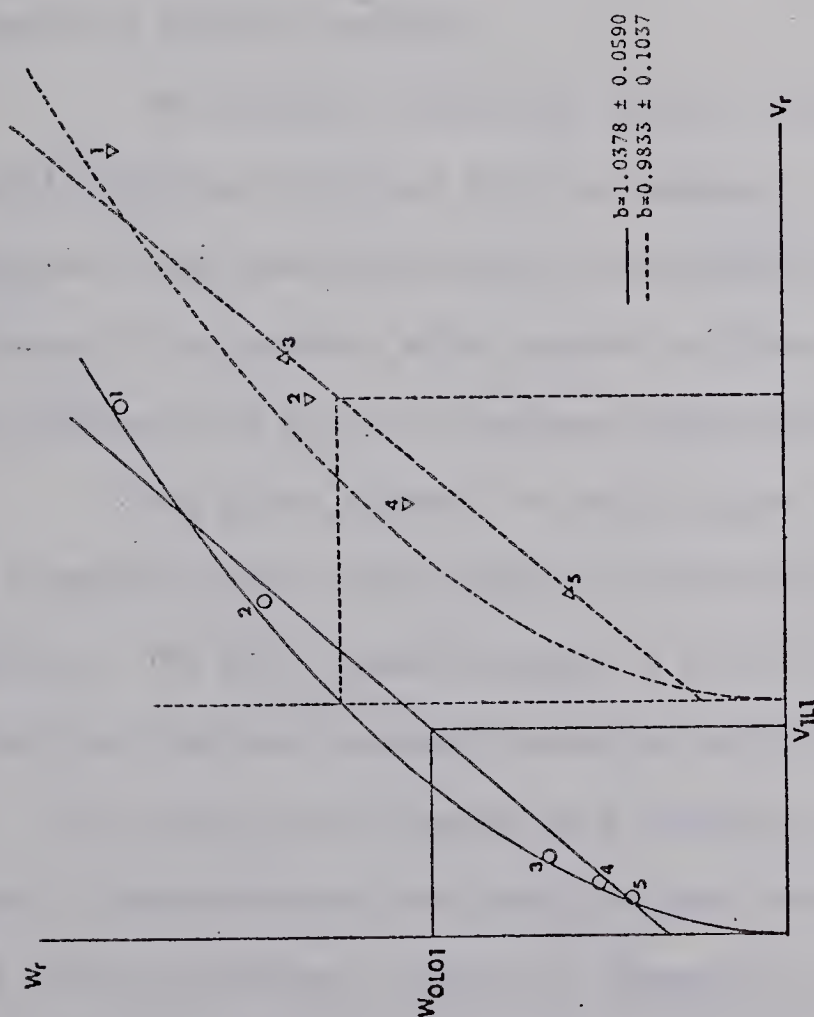


Figure 1. W_r , V_r graph for onset-of- heading from F_1 diallel set.

— $o = W_r$, V_r intercepts at Ellerslie
 --- $\Delta = W_r$, V_r intercepts at Parkland

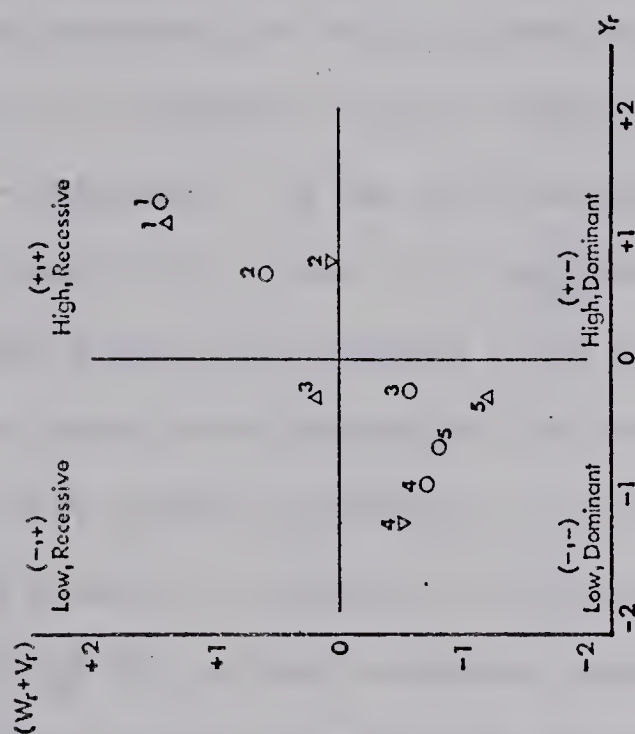


Figure 2. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for onset-of-heading from F_1 diallel set.

$o = Y_r$, $[W_r + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r$, $[W_r + V_r]$ intercepts at Parkland

that at both locations the highly recessive parent contributes towards late heading (+,+ quadrant) and the highly dominant one towards early heading (-,- quadrant). As far as other parents are concerned, Chinook and Ciano, lying in (+,+) and (-,-) quadrants, may be classified as recessive late headers and dominant early headers. Khush-hal's order of dominance seems to be affected by the environmental influence, being a dominant early header at Ellerslie (-,- quadrant) and a recessive medium-early header (-,+ quadrant) at Parkland. The number of groups of genes (h^2/H_2) ≈ 1 at both locations, suggests that at least one group of genes control onset-of-heading and exhibit dominance. The heritability estimates of 98.37% at Ellerslie and 66.42% at Parkland show that the character is highly heritable.

The results from Table 19 and 20 for final heading (Figures 3, 4) and heading-span (Figures 5,6) are subject to the same kind of interpretation as for onset-of-heading except for changes in the relative positions of the parents with respect to their ranking order for dominance, and therefore they are not discussed separately.

For plant height, the mean degree of dominance of 0.3 at both locations shows that height is inherited as a partially dominant character. The W_r, V_r graph (Figure 7) with a regression line intersecting the limiting parabola above its origin supports the above conclusion. The proportion of genes with positive and negative effects in the parents is approximately the same for both locations (0.158 at Ellerslie and 0.170 at Parkland), indicating asymmetry in the distribution of alleles at loci exhibiting dominance. The ratio of dominant to recessive

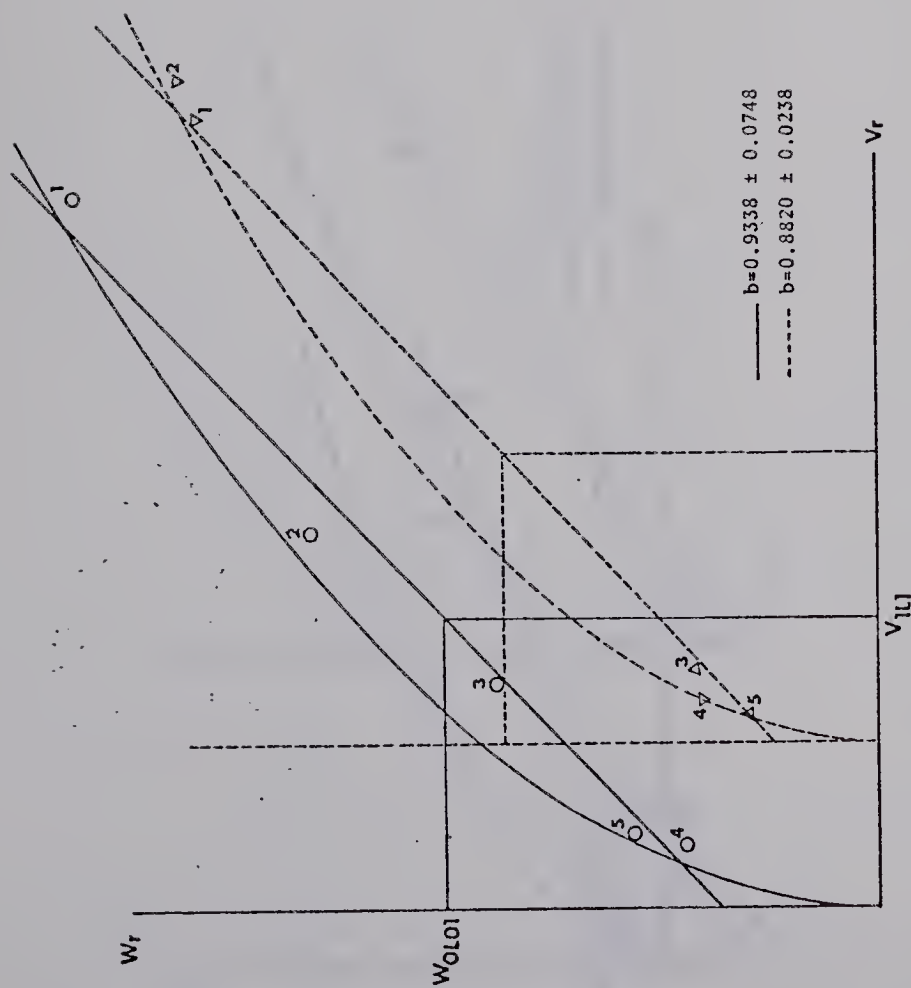


Figure 3. W_r , V_r graph for final heading from F_1 diallel set.

— $o = W_r$, V_r intercepts at Ellerslie
 --- $\Delta = W_r$, V_r intercepts at Parkland

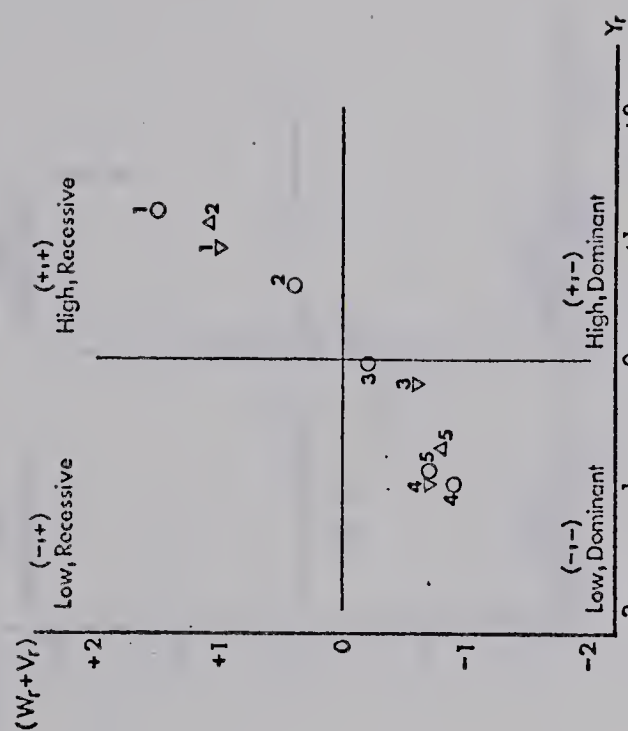


Figure 4. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for final heading from F_1 diallel set.

$o = Y_r$, $[W_r + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r$, $[W_r + V_r]$ intercepts at Parkland

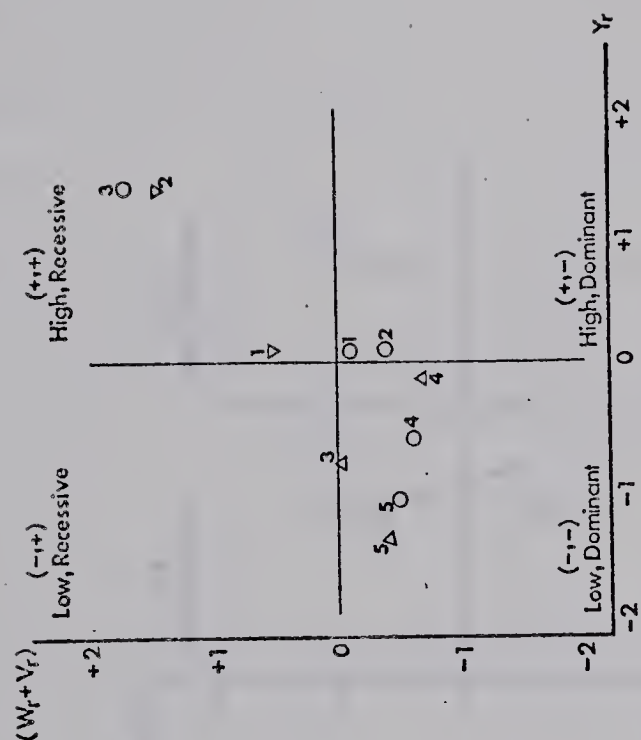


Figure 5. W_r , V_r graph for heading-span from F_1 diallel set.

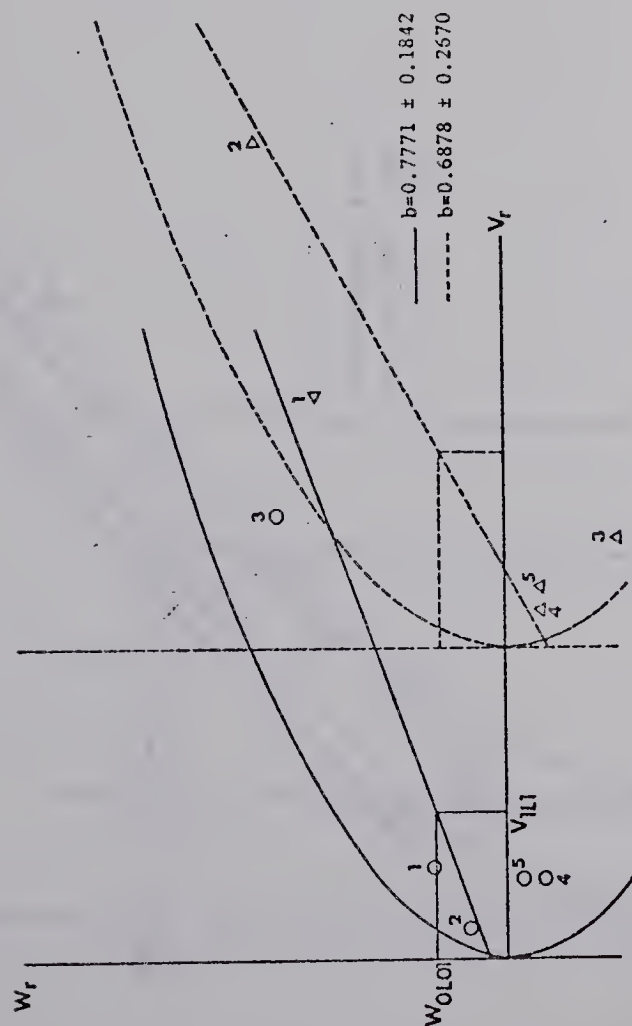


Figure 6. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for heading-span from F_1 diallel set.

$O = Y_r$, $[W_r + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r$, $[W_r + V_r]$ intercepts at Parkland

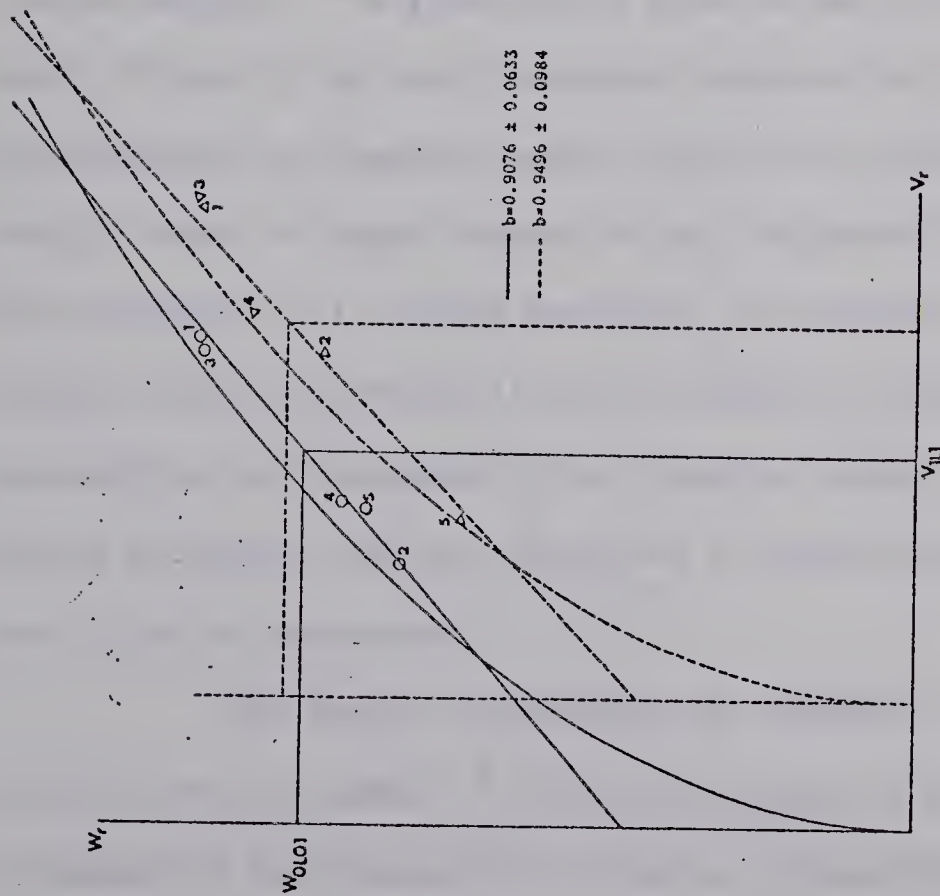


Figure 7. W_r , V_r graph for plant height from F_1 diallel set.

— $o = W_r$, V_r intercepts at Ellerslie
 --- $\Delta = W_r$, V_r intercepts at Parkland

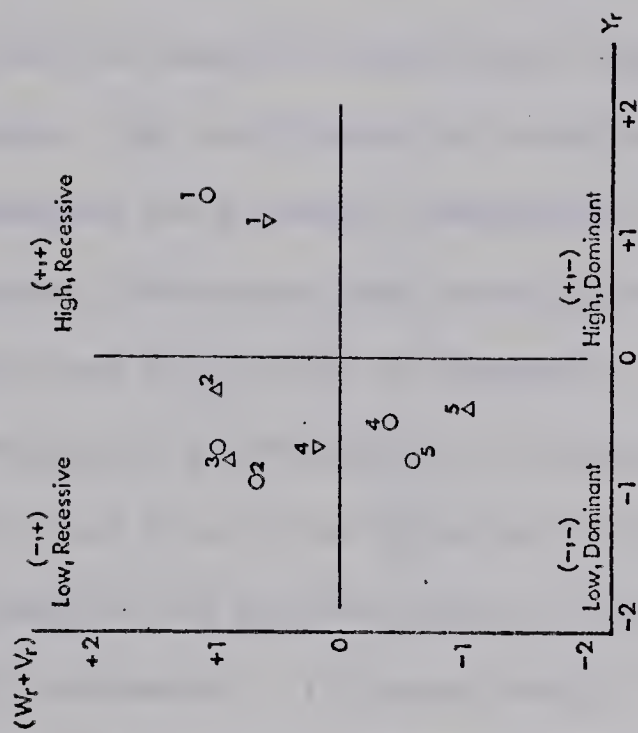


Figure 8. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for plant height from F_1 diallel set.

$o = Y_r$, $[W_r + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r$, $[W_r + V_r]$ intercepts at Parkland

genes in the parents is approximately equal to one at both locations, suggesting that the parents contain equal numbers of dominant and recessive genes. The coefficient of correlation between the parental order of dominance and parental measurements is 0.17 at Ellerslie and 0.07 at Parkland, indicating weak association between the measurements of the parents and their order of dominance. Figure 7 indicates that Marquis at Ellerslie and Khush-hal at Parkland are the most recessive parents while Inia at both the locations is the most dominant parent. Figure 8 classifies the parental order of dominance together with their height performance. It places highly recessive parents Marquis (at Ellerslie) and Khush-hal (at Parkland) into (+,+) and (-,+) quadrants, showing that recessiveness of the former is responsible for tallness, while the recessive genes of the latter carry effects decreasing height. The position of Inia in the (-,-) quadrant of the graph (Figure 8) at both locations suggests that it contains a preponderance of dominant genes contributing towards shortness. The ranking order of Ciano appears to be influenced by location effects. At Ellerslie, it is highly dominant, contributing towards reduced height while at Parkland it has an excess of recessive genes, again responsible for shortness. The character seems to be consistently highly heritable over the locations (77.40% heritability at Ellerslie and 82.99% at Parkland).

The genetic components of variation, D , F , H_1 and H_2 are not significant for number of tillers per plant at Ellerslie and therefore estimates of mean degree of dominance, proportion of dominant to

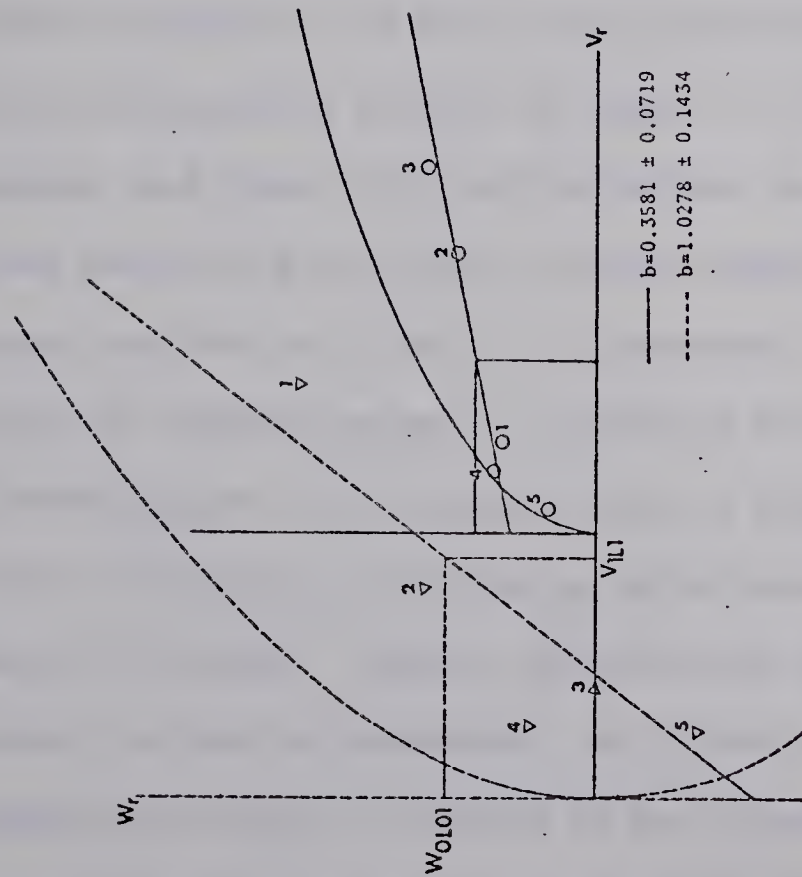


Figure 9. W_r, V_r graph for number of tillers per plant from F_1 diallel set.
 — $o = W_r, V_r$ intercepts at Ellerslie
 --- $\Delta = W_r, V_r$ intercepts at Parkland

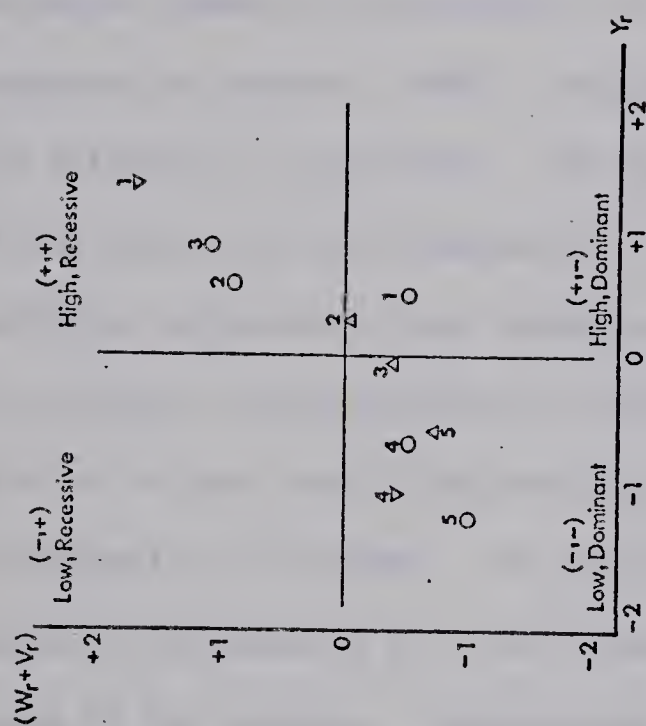


Figure 10. Standardized deviation graph of $[Y_r]$ $[W_r + V_r]$ for number of tillers per plant from F_1 diallel set.
 $o = Y_r, [W_r + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r, [W_r + V_r]$ intercepts at Parkland

recessive genes in the parents etc. should be meaningless (as suggested by Hayman, 1954b). Moreover, the W_r , V_r graph (Figure 9) for Ellerslie is distorted. The mean degree of dominance at Parkland (1.06) indicates over-dominance. This is supported by Figure 9 in which the regression line intersects the limiting parabola above its origin. The proportion of genes with negative and positive alleles at loci exhibiting dominance is 0.15 revealing asymmetry in distribution of alleles. The proportion of dominant to recessive genes in the parents is 3.409 which indicates an excess of dominant genes in the parents. Consequently Khush-hal, Ciano and Inia are categorized as parents with a preponderance of dominant genes, and of these Inia is the most dominant one as it lies closest to the point of intersection of the regression line with the limiting parabola (Figure 9). The significant positive correlation between the parental order of dominance and the parental measurements (0.80) shows that the genes with negative effects for number of tillers per plant are mostly dominant and those with positive effects are mostly recessive. This is shown graphically in Figure 10 where parental Y_r , $(W_r + V_r)$ intercepts occupy only the (+,+) and (-,-) quadrants. Ciano and Inia contain an excess of dominant genes (-,- quadrant) with lower tillering capacity. Chinook appears to be recessive, with a higher number of tillers per plant at Ellerslie, but shows an equal number of recessive and dominant genes at Parkland. Marquis and Khush-hal appear to be inconsistent with respect to order of dominance. At Ellerslie, Marquis has an excess of dominant genes but at Parkland it has become highly recessive. The reverse situation exists with Khush-hal which is placed in the (+,+)

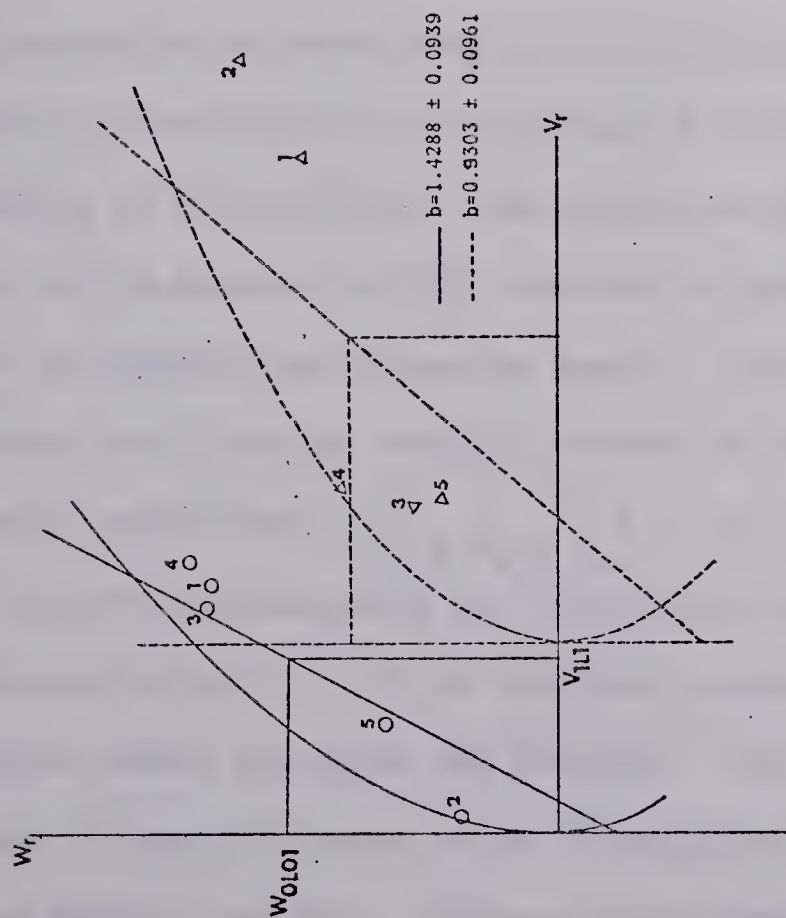


Figure 11. W_r , V_r graph for number of spikelets per spike from F_1 diallel set.

— $O = W_r$, V_r intercepts at Ellerslie
 --- $\Delta = W_r$, V_r intercepts at Parkland

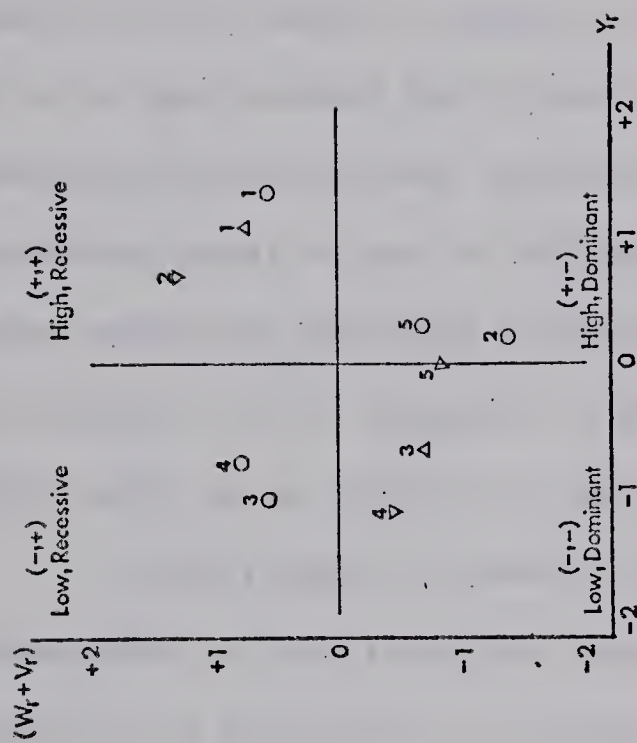


Figure 12. Standardized deviation graphs of $[Y_r]$ and $[W_r + V_r]$ for number of spikelets per spike from F_1 diallel set.

$O = Y_r$, $[W_r + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r$, $[W_r + V_r]$ intercepts at Parkland

quadrant at Ellerslie and in the $(-, -)$ quadrant at Parkland. The estimate for the number of groups of genes controlling tiller number seems to be questionable for Ellerslie (Table 20) where the relevant components of variation were nonsignificant (Table 19). However it is approximately equal to one at Parkland, showing that at least one group of genes exhibiting dominance controls tillering. The heritability of this character, low at Ellerslie (2.86%) and relatively high at Parkland (48.85%) seems to be affected by environmental differences.

With regard to number of spikelets per spike, there was over-dominance at both locations, since $[H_1/D]^{1/2} > 1$ and the W_r/V_r regression line intersects the limiting parabola below its origin (Figure 11). The genetic components of variation were not significant for Parkland and the proportional estimates of genetic parameters given in Table 20 have therefore to be ignored. For Ellerslie, the proportion of genes with positive and negative alleles at loci exhibiting dominance is approximately 0.2, indicating a slight asymmetry in distribution. The proportion of dominant to recessive genes in the parents is 0.99, suggesting approximately equal proportions of dominant and recessive genes. Figure 11 classifies Marquis, Khush-hal and Ciano as having an excess of recessive genes. The correlation coefficient $(r_{Y_r, W_r + V_r})$ of -0.2 at Ellerslie suggests that parental measurements are not related with their order of dominance, while $r = 0.75$ at Parkland suggests that genes for lower spikelet number per spike are dominant. Order of dominance of the parents (Figure 12) seems to be inconsistent for the two locations except Marquis and Inia. Chinook, the highly recessive parent at Parkland

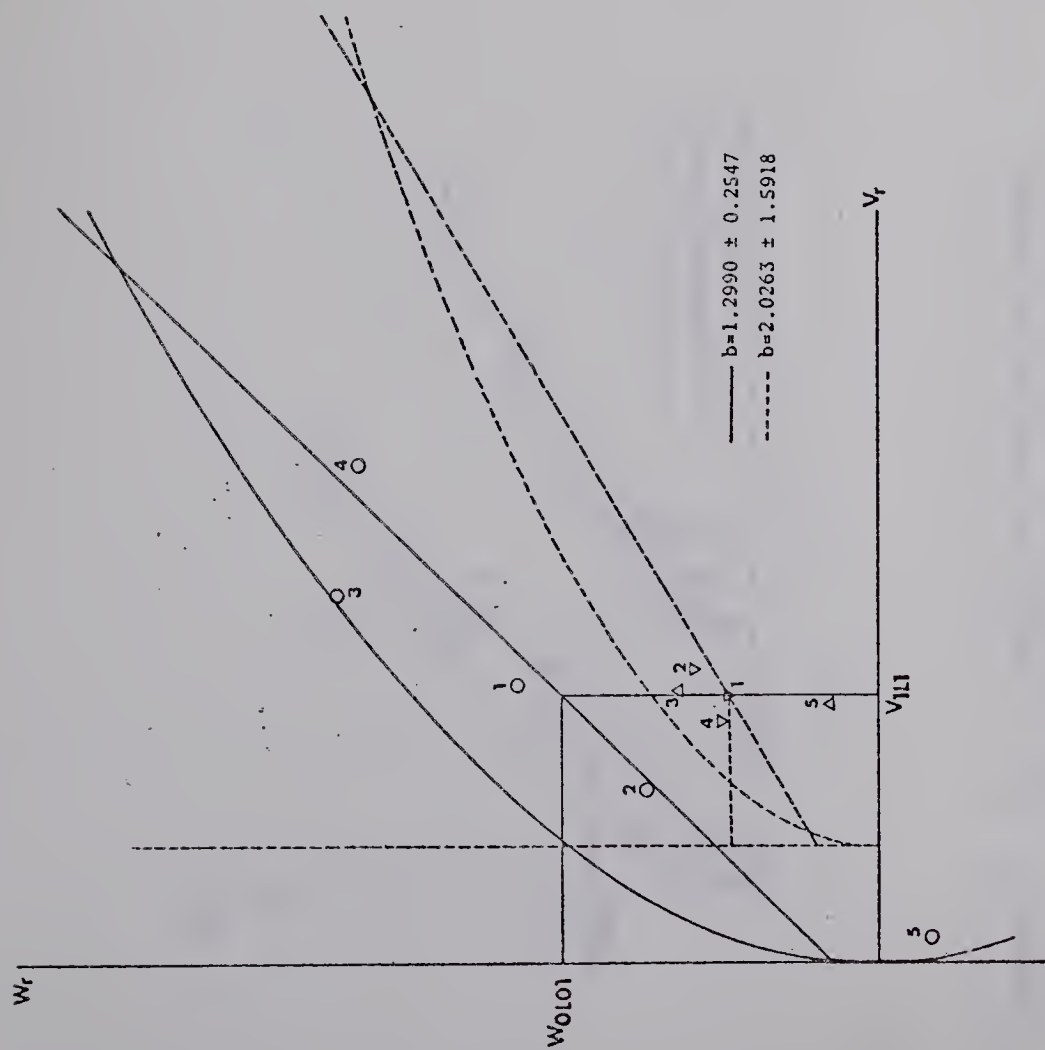


Figure 13. W_r , V_r graph for number of seeds per spike from F_1 diallel set.

— $o = W_r$, V_r intercepts at Ellerslie

--- $\Delta = W_r$, V_r intercepts at Parkland

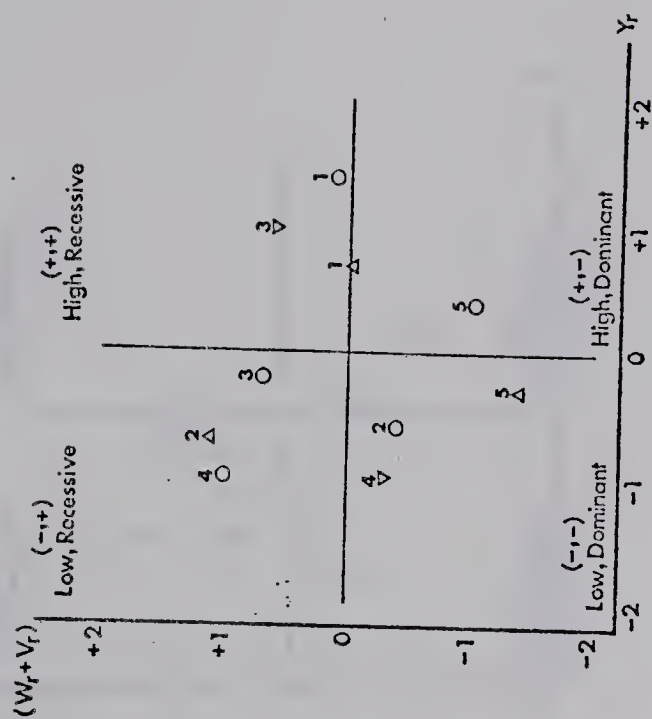


Figure 14. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of seeds per spike from F_1 diallel set.

$o = Y_r$, $[W_r + V_r]$ intercepts at Ellerslie

$\Delta = Y_r$, $[W_r + V_r]$ intercepts at Parkland

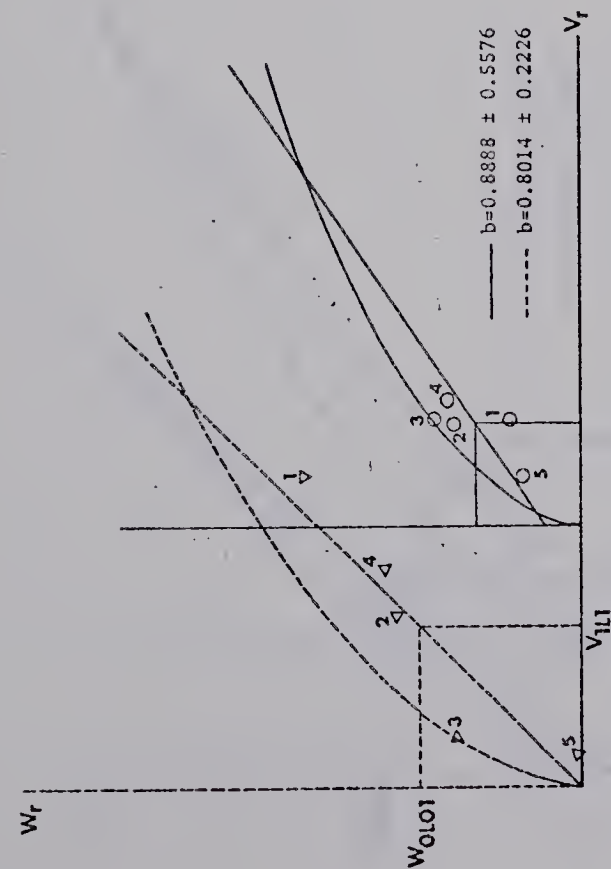


Figure 15. W_r , V_r graph for weight of seeds per spike from F_1 diallel set.
 — $o = W_r$, V_r intercepts at Ellerslie
 --- $\Delta = W_r$, V_r intercepts at Parkland

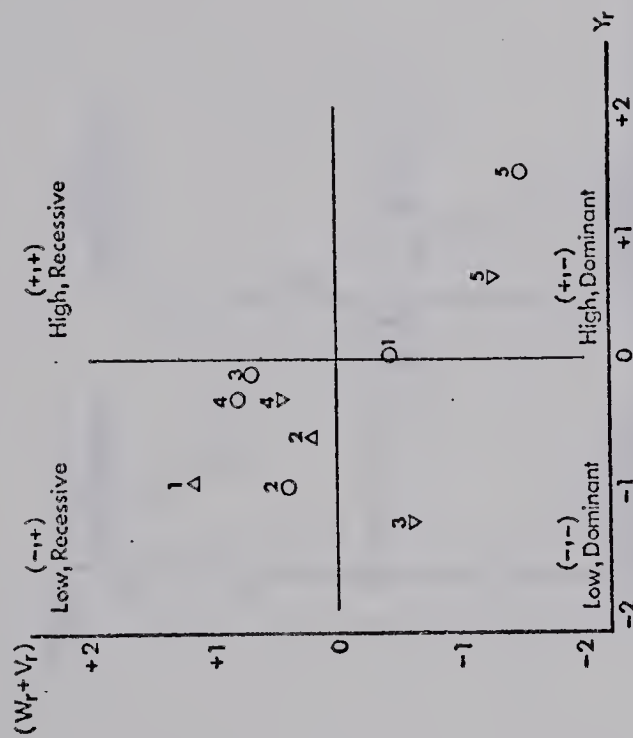


Figure 16. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for weight of seeds per spike from F_1 diallel set.
 $o = Y_r$, $[W_r + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r$, $[W_r + V_r]$ intercepts at Parkland

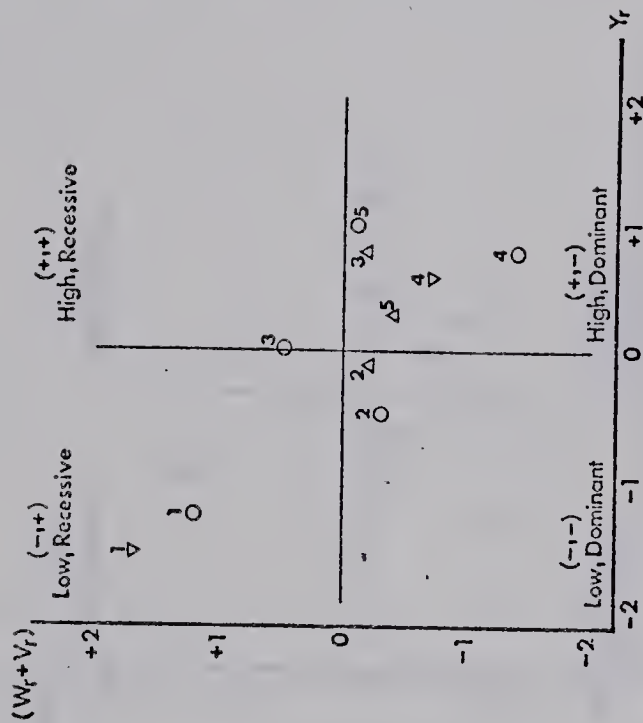


Figure 18. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for 1000-kernel weight from F_1 diallel set.

$o = Y_r, [W_r + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r, [W_r + V_r]$ intercepts at Parkland

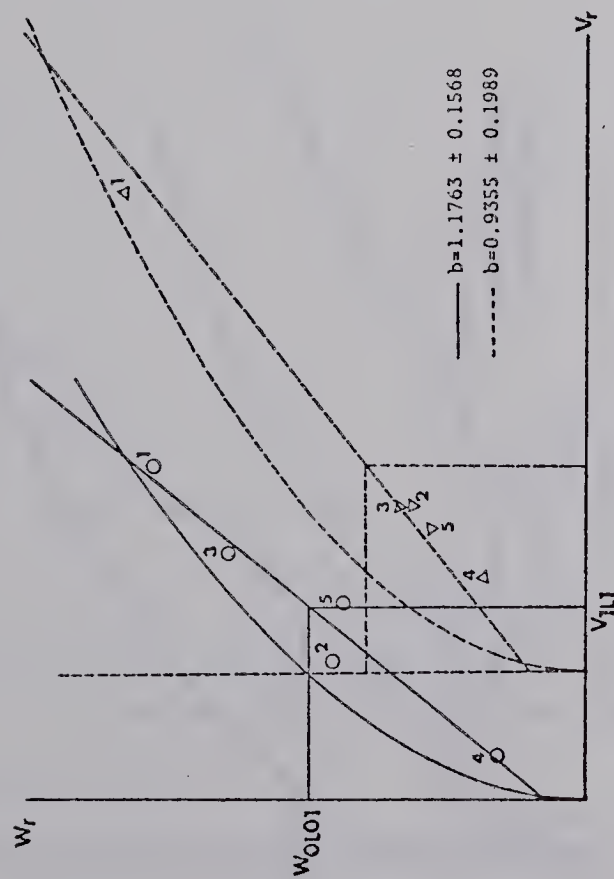


Figure 17. W_r, V_r graph for 1000-kernel weight from F_1 diallel set.

— $o = W_r, V_r$ intercepts at Ellerslie
 --- $\Delta = W_r, V_r$ intercepts at Ellerslie

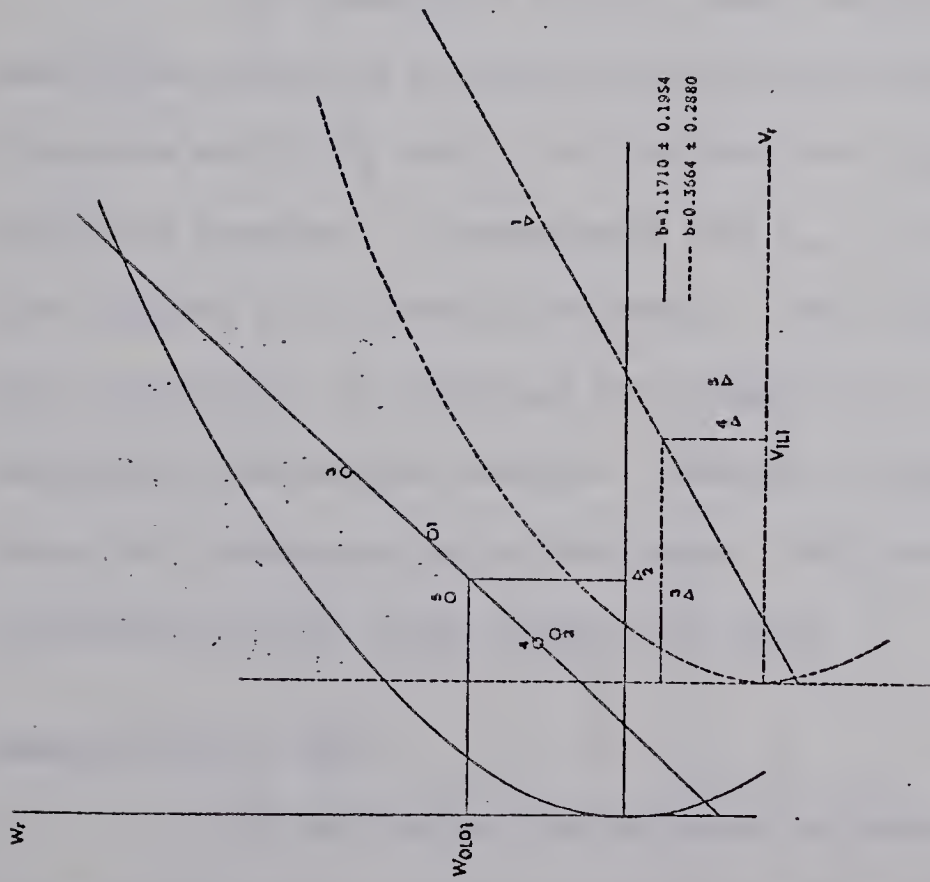


Figure 19. W_p, V_p graph for yield per plant from F_1 diallel set.
 — $o = W_p, V_p$ intercepts at Ellerslie
 --- $\Delta = W_p, V_p$ intercepts at Parkland

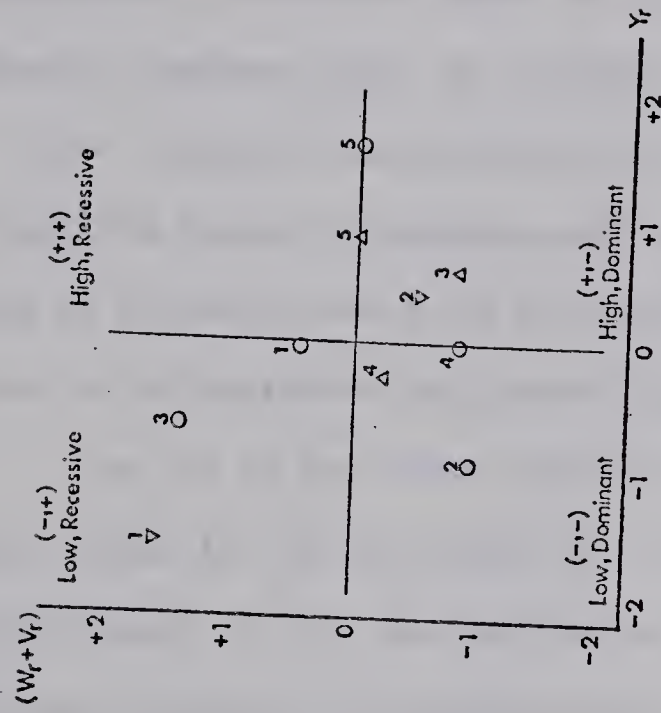


Figure 20. Standardized deviation graph of $[Y_p]$ and $[W_p + V_p]$ for yield per plant from F_1 diallel set.
 $o = Y_p, [W_p + V_p]$ intercepts at Ellerslie
 $\Delta = Y_p, [W_p + V_p]$ intercepts at Parkland

appeared highly dominant at Ellerslie. Khush-hal and Ciano with a preponderance of recessive genes at Ellerslie (-,+ quadrant) contained mostly dominant genes at Parkland (-,- quadrant). The ratio $h^2/H_2 = 0.46$ suggests that possibly one group of dominant genes is controlling the number of spikelets per spike. Heritability estimates of 31.82% at Ellerslie and 9.25% at Parkland suggest that not only the character is low heritable but inconsistent over the locations also.

As far as the other components of yield i.e. number of seeds per spike (Table 19, 20 and Figure 13, 14), weight of seeds per spike (Table 19, 20 and Figure 15, 16) and 1000-kernel weight (Table 19, 20 and Figure 17, 18) are concerned, the interpretation of the results from relevant tables and figures will be similar. The changes in the relative positions of the parents for their order of dominance may be encountered which may be interpreted accordingly.

The results of diallel cross analysis for yield per plant are meaningless both for Ellerslie and Parkland data. Paradoxically, H_1 for Ellerslie and D , H_1 and H_2 for Parkland have negative values significantly different from zero. Consequently the V_r , W_r graph (Figure 19) for Parkland appears to be severely distorted. The respective graph for Ellerslie does not seem to be distorted and suggests the validity of the hypotheses underlying the diallel analysis. However, a significant negative H_1 invalidates the interpretation of the graph. The same objection applies to standardized deviation graph (Figure 20) also.

ANALYSIS OF F_2 DATA

It will not be out of place to mention again that the F_2 generation hybrids were duplicated in each replication at both locations,

TABLE 21

Simple correlation coefficients between ten characters
from F_2 diallel set at two locations.

Character	1	2	3	4	5	6	7	8	9	10
1. Onset-of-heading	-	0.382** 0.831**	0.115 -0.040	0.763** 0.798**	0.196 0.522**	0.433** 0.536**	0.275* 0.306**	-0.274* -0.400**	-0.610** -0.686**	-0.249* -0.126
2. Final heading		-	0.025 0.522**	0.253* 0.750**	0.176 0.556**	0.142 0.516**	0.087 0.234*	-0.114 -0.398**	-0.229* -0.638**	-0.021 -0.089
3. Heading-span			-	0.302** 0.122	0.166 0.205	0.027 0.102	-0.074 -0.049	-0.299** -0.102	-0.322** -0.095	-0.201 0.037
4. Plant height				-	0.394** 0.506**	0.575** 0.652**	0.263* 0.248*	-0.287* -0.412**	-0.633** -0.687**	0.009 -0.034
5. Number of tillers per plant					-	0.204 0.353**	0.081 0.060	-0.032 -0.278*	-0.113 -0.505**	0.565** 0.238*
6. Number of spikelets per spike						-	0.625** 0.444**	0.218 0.192	-0.346** -0.349**	0.267* 0.329**
7. Number of seeds per spike							-	0.657** 0.160	-0.130 -0.141	0.259* 0.065
8. Weight of seeds per spike								-	0.650** 0.701**	0.392** 0.473**
9. 1000-kernel weight									-	0.252* 0.265*
10. Yield per plant										-

First reading under each column refers to Ellerslie and second to Parkland.

* Significant at 5% level

** Significant at 1% level

partly to meet the entry requirements of the partially balanced lattice design, and partly to reduce the genetic sampling error inherent in the segregating generation. Though the heading data and yield observations were recorded separately for the two repetitions, the analysis of the data is based on their average.

Simple correlation coefficients for all the characters are shown in Table 21. The results reveal that:

Onset-of-heading was positively correlated with final heading, plant height, number of spikelets per spike, number of seeds per spike, and negatively correlated with weight of seeds per spike, 1000-kernel weight and yield per plant at both locations. Correlation with number of tillers per plant was only exhibited at Parkland. The negative association of onset-of-heading with yield and its two components, weight of seeds per spike and 1000-kernel weight, suggests that early maturing varieties are higher yielders and consequently their seed weighs more than the late maturing ones. This kind of relationship was also noticed for F_1 hybrids. Correlation of final heading and heading-span with other characters has the same kind of interpretation.

Plant height exhibited significant positive correlation with number of tillers per plant, number of spikelets per spike, number of seeds per spike and 1000-kernel weight at both locations. Correlation with yield per plant was not significant.

Number of tillers per plant exhibited positive correlation with yield per plant at both locations and with number of spikelets per spike at Parkland but was negatively associated with weight of seeds per

TABLE 22

Varimax rotated factor matrix for ten characters
from F₂ diallel set at two locations.

Character	Communality	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5
Onset-of-heading	0.977 0.886	0.958 0.896	0.149 0.023	-0.047 0.253	-0.178 -0.116	-0.055 -0.075
Final heading	0.981 0.940	0.895 0.794	0.129 0.001	-0.029 0.252	-0.208 -0.090	0.346 0.488
Heading-span	0.996 0.993	0.152 0.050	-0.051 -0.036	0.009 0.071	-0.140 0.019	0.975 0.992
Plant height	0.851 0.889	0.746 0.922	0.267 0.012	0.250 0.194	-0.372 -0.004	0.148 0.049
Number of tillers per plant	0.912 0.917	0.277 0.351	-0.039 0.013	0.903 0.848	-0.006 0.235	0.133 0.142
Number of spikelets per spike	0.834 0.883	0.288 0.688	0.811 0.590	0.162 0.046	-0.257 0.233	-0.022 0.071
Number of seeds per spike	0.903 0.981	0.186 0.156	0.904 0.967	0.039 0.098	0.221 0.049	-0.014 -0.050
Weight of seeds per spike	0.994 0.943	-0.234 -0.381	0.581 0.725	0.082 -0.346	0.760 0.391	-0.129 -0.024
1000-kernel weight	0.913 0.880	-0.462 -0.625	-0.155 0.059	0.072 -0.546	0.802 0.411	-0.162 -0.005
Yield per plant	0.898 0.929	-0.285 -0.045	0.278 0.252	0.839 0.129	0.105 0.920	-0.156 0.008
% of total variability explained	92.590 92.399	28.424 34.420	20.287 18.768	16.261 13.540	15.814 13.089	11.805 12.581

First reading under each column refers to Ellerslie and second to Parkland

spike and 1000-kernel weight at Parkland. Negative correlations with weight of seeds per spike and 1000-kernel weight establish an inverse relationship indicating that more the tillers per plant, the higher is the yield and the lower the weight of seeds per spike and 1000-kernel weight. The correlation coefficients of other components of yield, viz., number of spikelets per spike, number of seeds per spike, weight of seeds per spike and 1000-kernel weight may be explained in the same manner.

Yield per plant was positively correlated with its components, viz., number of tillers per plant, number of spikelets per spike, weight of seeds per spike and 1000-kernel weight. It was negatively associated with onset-of-heading at Ellerslie, while its correlation at Parkland was not significant. Negative correlation of yield with onset-of-heading indicates that high yielding varieties are usually early maturing.

Factor analysis was performed on the complete F_2 diallel data. Four principal factors, derived by factorizing correlation matrix into a varimax rotated factor matrix, accounted for 81.7% of the variability present in the data. Since it was thought that 82% of the variation (as explained by these four factors) was not sufficient, the number of factors was raised to five and the procedure was repeated through computerization. The five factors were found to explain 92% of the variation in the data. A further six factor matrix explained 96% of the variability, it was not significantly different from the five factor-matrix which was therefore considered and the results are given in Table 22.

Since the first factor showed the highest loadings for

onset-of-heading and final heading at both locations and accounted for 28%^{of} variability at Ellerslie and 34% at Parkland, it was named *lateness*.

It was positively affected by plant height and negatively by weight of seed per spike, 1000-kernel weight and yield per plant at both locations. This implies that a longer heading period causes the plants to grow taller but yield less, with lower seed weight per spike and consequently lower 1000-kernel weight. Number of tillers per plant, number of spikelets per spike and number of seeds per spike at both locations contributed very little to this factor.

The second principal component was termed *yield-components*. Although earlier the term *yielding-capacity* was applied in the F_1 factor analysis, the above term is considered more suitable because of the consistently higher loadings for yield components. Thus this component shows maximum loadings for number of spikelets per spike, number of seeds per spike and weight of seeds per spike at both locations. Negative contributions towards this factor due to heading-span at both locations and number of tillers per plant and 1000-kernel weight at Ellerslie reveal that varieties with longer maturing times yield less, produce fewer tillers per plant and show lower 1000-kernel weight.

The third principal component was named *tillering-capacity* as it provided the maximum contribution to number of tillers per plant at both locations. The factor accounted for 16% and 13.5% of the total variability in the data at Ellerslie and Parkland respectively. Yield was significantly affected at Ellerslie, but at Parkland, the contribution towards yield was comparatively low. Number of spikelets per spike,

TABLE 23

Estimates of general combining ability of five parental lines used in F_2 diallel set for ten characters at two locations.

Character	Marquis	Chinook	Khush-hal	Ciano	Inia
Onset-of-heading	1.8000 2.2267	1.3167 2.0267	-0.3667 -1.0900	-1.6833 -2.0066	-1.0667 -1.1566
Final heading	1.9767 2.0334	1.5767 2.5667	-0.0733 -0.9167	-1.9733 -2.0333	-1.5066 -1.6570
Heading-span	0.1500 -0.2033	0.3667 0.5467	0.2667 0.1800	-0.3167 -0.0367	-0.4667 -0.4867
Plant height	13.3708 12.9892	10.0921 12.0445	-6.7329 -7.7827	-7.3467 -9.2980	-9.3831 -8.9530
Number of tillers per plant	-0.0055 0.8860	0.4139 0.6827	0.4435 0.5310	-0.2707 -0.9973	-0.8512 -1.1023
Number of spikelets per spike	0.7264 0.6867	0.2257 0.4672	-0.6356 -0.3060	-0.4576 -0.7084	0.1412 -0.1394
Number of seeds per spike	3.1883 2.2384	-1.5763 -1.1155	-1.7061 0.2738	-2.1989 -2.4832	2.2930 1.0865
Weight of seeds per spike	0.0283 -0.0274	-0.1592 -0.1023	-0.0475 +0.0665	-0.0079 -0.0431	0.1863 0.1063
1000-kernel weight	-2.0321 -2.2536	-2.2150 -1.3656	0.4223 1.2445	1.7856 1.2144	2.0392 1.1603
Yield per plant	0.0508 -0.5307	-1.4712 0.1256	-0.7275 0.6319	0.6961 -0.5374	1.4518 0.3109

First reading under each column refers to Ellerslie and second to Parkland.

number of seeds per spike and heading-span at both locations , weight of seeds per spike and 1000-kernel weight at Ellerslie contributed positively to this factor.

The fourth principal factor, accounting for 15% and 13% variability at Ellerslie and Parkland and carrying the highest loadings for 1000-kernel weight at both locations, was called *kernel-weight*. The factor was contributed to by weight of seeds per spike and yield per plant at both locations, although the effect of number of seeds per spike appears to be slight. Other characters such as plant height, final heading and onset-of-heading at both locations were negatively affected.

The fifth principal factor, since it was termed *heading period*, was strongly affected by heading-span. It explained 12% of the total variation at both locations, and was adversely affected by yield and its components. Final heading, plant height and number of tillers per plant at both locations scored positively for this factor but their contribution was relatively low.

Combining ability analysis

Estimates of general combining ability for the five parental lines are presented in Table 23. Marquis scored highest for onset-of-heading and Ciano lowest at both locations. The same was true for final heading. For heading-span, Chinook ranked first and Ciano last. In plant height, Marquis excelled at both locations while Inia at Ellerslie and Ciano at Parkland were lowest. For number of tillers per plant, Khush-hal ranked first at Ellerslie and Chinook ranked first at Parkland.

TABLE 24 Onset-of-heading

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano			
Marquis	-	-0.0500 1.2066	-1.1166 -0.2600	-0.7166 -1.5100	1.8000 2.2267	3.1762 4.8224	-0.1594 -0.3394
Chinook	-0.3333 0.1667	-	-0.4667 -0.6434	-0.7333 0.1900	1.3167 2.0267	1.6699 3.9718	-0.1586 0.1459
Khush-hal	-0.4167 -0.4167	-0.4167 0.1667	-	0.1167 -0.3600	-0.3667 -1.0900	0.0707 1.0522	0.3288 -1.1789
Ciano	0.0 -0.4167	0.8333* 0.2500	0.3333 -0.2500	- 0.5667 1.2066	-1.6833 -2.0066	2.7697 3.8908	0.1956 0.4759
Inia	0.0833 -0.6667	0.6667 -0.0833	0.3333 -0.2500	0.4167 -0.4167	-1.0067 -1.1556	1.0740 1.2020	0.3537 2.0317

TABLE 25 Final heading

Marquis	-	0.2233 1.0167	-1.1267 -1.3833	-0.6434 -1.4333	-1.0267 -1.2333	1.9767 2.0334	-0.1441 -0.5093
Chinook	-0.0833 0.5833	-	0.3566 -1.8333	-1.0767 -0.8000	-0.2100 -1.6833	1.5767 2.5667	-0.1275 -0.0158
Khush-hal	-0.0833 0.3333	-0.6667 0.2500	-	-0.3434 0.5167	-0.5600 0.3000	-0.0733 -0.9167	0.3214 1.2490
Ciano	-0.6667 -0.1667	0.6667 -0.3333	0.4167 -0.6667	-	1.2567 1.0833	-1.9733 -2.0333	0.4196 0.4779
Inia	0.7500* -0.0833	0.6667	0.3333 0.3333	0.4167 -0.6667	-	-1.5066 -1.6500	0.8529 1.3635

First reading under each column refers to Ellerslie and the second to Parkland.
*Significant at 5% level

Estimates of specific combining ability, reciprocal effects and variances
of general and specific combining ability from F_2 diallel set at two locations.

TABLE 26. Heading-span

♀ Parent	Specific combining ability					GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis	-	0.1667 0.0200	0.0167 -1.1133	0.1000 0.0200	-0.0833 -0.1133	0.1500 -0.2033	-0.0443 -0.2013	-0.1671 -0.6067
Chinook	0.2500 0.4167	-	0.7167 -1.1967	-0.4500 -0.9800	0.2000 0.1367	0.3667 0.5467	0.0676 0.0562	-0.1578 -0.6065
Khush-hal	0.3333 0.7500	-0.2500 0.0833	-	-0.4333 0.8867	-0.8667 1.3367	0.2667 0.1800	0.0043 -0.2103	0.0042 0.2838
Ciano	-0.6667 0.3333	-0.1667 -0.5833	0.0833 -0.4167	-	0.7167 -0.1133	-0.3167 -0.0367	0.0334 -0.2413	-0.0337 -0.0243
Inia	0.6667 0.5833	0.0 0.2500	0.0 0.5833	0.0 -0.2500	-	-0.4667 -0.4867	0.1509 -0.0058	0.2701 0.0037

TABLE 27. Plant height

Marquis	-	2.8015 1.8702	0.0336 5.4357	-1.9122 -1.9114	-5.2829 -6.1106	13.3708 12.9892	177.5788 166.6538	-2.9988 -5.1606
Chinook	-1.1342 2.0642	-	1.3486 1.2654	-3.5393 -1.3834	2.7586 0.2390	10.0921 13.0445	100.6507 168.0942	-0.9129 -3.9947
Khush-hal	3.3558* 0.8525	1.7808 3.4392	-	1.3133 0.1846	-0.2195 -2.8154	-6.7329 -7.7827	44.1325 58.5057	-2.3549 5.2222
Ciano	-0.8783 0.0633	3.8492* 5.0650*	0.0467 0.0592	-	1.0260 1.3933	-7.3467 -9.2980	52.7748 84.3886	2.9703 -3.2934
Inia	12.9255** 8.2025**	5.8667** 5.3258*	-0.2958 -0.4642	1.5775 -0.7742	-	-9.3831 -8.9530	86.8439 78.0926	9.5876 10.5941

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 1% level

** Significant at 5% level

For number of spikelets per spike, Marquis was highest at both locations while Khush-hal at Ellerslie and Ciano at Parkland ranked lowest. For number of seeds per spike, Marquis ranked highest at both locations and Ciano was the lowest. For weight of seeds per spike and 1000-kernel weight, Inia ranked first at both locations, while Chinook ranked last for weight of seeds per spike; and for 1000-kernel weight, Marquis at Parkland and Chinook at Ellerslie ranked last. For yield, Inia at Ellerslie and Khush-hal at Parkland scored highest GCA and Khush-hal at Ellerslie and Ciano at Parkland ranked lowest.

Specific combining abilities of the F_2 hybrids, the reciprocal effects and the variances for general and specific combining abilities are given in Tables 24 to 33. These are discussed under individual characters.

Cross (CxI) had the highest SCA for onset-of-heading (Table 24) at both locations and (MxK) at Ellerslie and (MxI) at Parkland were the lowest. Hybrid (CxI) with the highest SCA had parents with the lowest GCA's at both locations. Similarly the lowest ranking hybrids (MxK) and (MxI) had one parent (Marquis) with the highest GCA at both locations. These kinds of results support those of the F_1 combining ability analyses. Thus it is seen that parental lines with high GCA's do not necessarily produce hybrids with high SCA's. The variances for GCA were usually larger than those for SCA except for Khush-hal at Ellerslie and Inia at Parkland. Relatively high SCA variances for Inia and Khush-hal imply an inconsistency in their SCA performance of their hybrids at both locations. Reciprocal effects were generally non-significant except for (CxCH) at Ellerslie which may be ascribed to the female parent of the hybrid.

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F_2 diallel set at two locations.

TABLE 28. Number of tillers per plant

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano			
Marquis	-	0.0155 -0.7810	-0.5067 -0.5043	0.05200 -0.6510	-0.0055 0.8860	-0.1858 0.5798	-0.4646 -0.5129
Chinook	-0.0833 -0.3583	-	0.4832 0.9407	-0.9860 -0.2310	0.7246 0.6827	0.4139 0.2609	-0.4646 -0.3096
Khush-hal	0.7260 -1.0667	0.5167 0.1750	-	0.8520 -0.2043	0.4435 0.5310	0.0108 0.0768	-0.3012 -0.1332
Ciano	-0.4185 0.6250	0.3667 0.8583	0.5158 -0.0167	-	-0.2707 -0.9973	-0.1126 0.7895	0.1023 -0.3400
Inia	0.8230 0.0667	0.7500 0.1250	0.2437 0.0333	0.4908 -0.0500	-0.5812 -1.1023	0.1520 1.0100	0.0947 -0.4188

Reciprocal effects

TABLE 29. Number of spikelets per spike

Marquis	-	-0.0184 0.5606	0.3592 0.1479	-0.2315 0.1164	-0.0934 -0.1162	0.7264 0.6867	-0.1169 -0.1167
Chinook	0.8083* 0.0222	-	-0.0646 0.4920	-0.1672 -0.3278	0.5422 -0.1107	0.2257 0.4672	-0.1168 -0.0629
Khush-hal	-0.2523 -0.0472	-0.0500 0.3832	-	0.3346 -0.3072	-0.5709 -0.1203	-0.6356 -0.3060	-0.0725 -0.0796
Ciano	-0.0117 -0.0870	0.1972 -0.2613	0.2123 0.2750	-	0.1783 0.2484	-0.4576 -0.7084	-0.0524 -0.0959
Inia	0.4678 0.3723	0.1057 0.0473	-0.3203 0.1305	-0.1243 0.0418	-	0.1412 -0.1394	0.1033 -0.1337

First reading under each column refers to Ellerslie and the second to Parkland.

*Significant at 5% level

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F_2 diallel set at two locations.

TABLE 30. Number of seeds per spike

♀ Parent	Specific combining ability					GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis	-	1.1545 0.2870	-0.7005 -0.0244	0.1160 1.3941	0.5999 0.6768	3.1883 2.2384	9.3728 4.0955	-1.9670 -2.2876
Chinook	0.7028 0.1278	-	0.0982 0.0492	-0.0284 -0.1192	2.0048 0.7419	-1.5763 -1.1155	1.6979 0.3293	-1.5227 -2.2601
Khush-hal	0.1287 -1.2997	-1.4832 0.0360	-	0.2428 -1.8748	-1.4129 -0.5793	-1.7061 0.2738	2.1238 -0.8401	-1.8002 -2.2866
Ciano	0.7217 0.7168	0.9697 -1.2167	-0.1442 0.3277	-	1.3696 0.7678	-2.1989 -2.4832	4.0483 5.2511	-1.9426 -0.4635
Inia	1.7125 0.9752	-0.0612 0.4083	1.0087 -0.7652	0.5783 1.0390	-	2.2930 1.0865	4.4710 -0.2653	0.7809 -1.6431

Reciprocal effects

TABLE 31. Weight of seeds per spike

Marquis	-	-0.0530 0.0068	0.0072 -0.0384	0.0107 0.0898	0.1000 0.1372	0.0283 -0.0274	-0.0017 -0.0018	-0.0064 -0.0063
Chinook	0.0022 0.0172	-	-0.0560 -0.0018	0.0218 -0.0060	0.0196 -0.0131	-0.1592 -0.1023	0.0228 0.0079	-0.0054 -0.0063
Khush-hal	-0.0283 -0.0558	-0.0740 -0.0208	-	0.0447 -0.0383	-0.0299 0.0114	-0.0475 0.0665	-0.0003 0.0019	-0.0053 -0.0058
Ciano	0.1072 0.0700	0.0355 -0.0573	-0.0413 -0.0225	-	-0.0030 0.0051	-0.0079 -0.0431	-0.0025 -0.0007	-0.0055 -0.0031
Inia	0.0237 0.0885	0.0072 -0.0143	-0.0377 -0.0503	-0.0052 0.0277	-	0.1863 0.1063	0.0322 0.0088	-0.0026 0.0001

First reading under each column refers to Ellerslie and the second to Parkland.

With respect to final heading (Table 25) and heading-span (Table 26), although there are some differences in relative positions of the parents and hybrids concerned, the general conclusions are the same as for onset-of-heading.

Cross (MxCH) at Ellerslie and (MxK) at Parkland ranked highest for plant height while (MxI) at both locations was the lowest (Table 27). Cross (MxCH) had both parents with highest GCA's at both locations while cross (MxK) with highest SCA at Parkland had one parent (Khush-hal) with a comparatively low GCA. Similarly (MxI) with lowest SCA at both locations had Marquis parent with highest GCA at both locations. In all cases the variances for GCA were greater than those for SCA. Crosses (CxCH), (IxM) and (IxCH) at both locations and (KxM) at Ellerslie showed significant reciprocal effects, which may be ascribed to the female parents because of the positive sign appended to each effect.

For number of tillers per plant (Table 28), crosses (KxC) at Ellerslie and (CHxK) at Parkland scored highest in SCA and (CHxC) at Ellerslie and (MxCH) at Parkland scored lowest. It is again noteworthy that one parent of the hybrids with high SCA (Ciano) had the second lowest GCA at both locations, while one parent of those scoring lowest in SCA (Chinook) had the highest GCA at both locations. The variances for GCA were, in general, greater than those for SCA and the reciprocal effects were non-significant.

The general interpretations for the remaining components of yield, viz., number of spikelets per spike (Table 29), number of seeds per spike (Table 30), weight of seeds per spike (Table 31) and 1000-kernel

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F_2 diallel set at two locations.

TABLE 32. 1000-kernel weight

Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano			
Marquis	-	-0.0159 -0.2108	0.2364 -0.8323	-0.1336 1.4480	1.4490 2.2354	-2.0321 -2.2536	-1.7115 -1.4056
Chinook	-0.5203 0.2470	-	-1.4490 0.1446	0.4314 -0.2289	-1.1334 -0.7060	-2.2150 -1.3656	-1.7114 -1.3909
Khush-hal	-1.2750 -0.2907	-0.4182 -0.5318	-	0.9701 0.3904	0.9718 0.9605	0.4223 1.2445	-0.9926 -1.1678
Ciano	1.6177 0.2192	0.0647 -0.3352	-1.0387 -0.0517	-	-1.8572 0.3992	1.7856 1.2144	-1.3299 -0.6385
Inia	-0.7592 1.0892	0.1358 -0.5033	-0.8753 -0.2993	-0.6647 -0.3512	-	2.0392 1.1603	0.3453 0.7868

TABLE 33. Yield per plant

Marquis	-	0.5420 -0.8039	-0.8646 0.7455	1.1590 0.0267	-0.1661 0.7448	0.0508 -0.5307	-0.9980 -1.0655
Chinook	-0.4107 0.6045	-	0.1689 1.3541	-1.0782 -0.7700	0.1929 0.3538	-1.4712 0.1256	-0.9001 -0.8501
Khush-hal	2.1502* -1.5562	0.5530 -0.0635	-	1.7764 0.0255	-0.4546 -1.2061	-0.7275 0.6319	-0.7394 -0.2690
Ciano	-0.9003 1.3395	-0.1892 -0.1583	-0.4672 -0.2452	-	0.0659 0.1652	0.6961 -0.5374	0.8891 -0.8674
Inia	1.0152 0.5628	1.1928 -0.4918	0.6962 -0.3988	-0.4528 -0.1468	-	1.4518 0.3109	-0.9061 -0.3448

First reading under each column refers to Ellerslie and the second to Parkland.

*Significant at 5% level

weight (Table 32) and the conclusions derived therefrom with respect to SCA's do not differ from number of tillers per plant. Only the relative positions and respective ranking orders of the parents and hybrids are changed.

For yield per plant (Table 33), crosses (KxC) at Ellerslie and (CHxK) at Parkland, respectively scored highest in SCA while (CHxC) at Ellerslie and (KxI) at Parkland ranked lowest. One parent of (KxI), Inia, scored highest for GCA at both locations while one parent of (CHxC), Chinook, scored lowest at Ellerslie and other parent, Ciano, scored second highest at Ellerslie. (KxC) had one parent (Khush-hal) with the second lowest GCA at Ellerslie. The variances for GCA were greater than those for SCA except for Marquis and Ciano at both locations, and Chinook, Khush-hal and Inia at Parkland. The reciprocal effects were non-significant except for (KxM) at Ellerslie which may be ascribed to Khush-hal because of the positive sign appended to the effect.

The following conclusions may be drawn from the analysis of general and specific combining ability for all the characters considered: (1) In all cases, since hybrids with high SCA's were associated with the parents with low GCA's, the high GCA's of the parental lines may not be taken as criteria to predict high SCA's of their hybrids. (2) In most cases, the variances for GCA's were greater than those for SCA's. The analysis of variance for general and specific combining ability (Table 34) also supports this conclusion. In all cases, the mean squares for GCA in Table 34 are significant except for heading-span and yield per plant at Parkland. This implies that GCA which is largely due to

TABLE 34

Analysis of variance of general and specific combining ability and reciprocal effects from F₂ diallel set for ten characters at two locations.

Character	M.S. for GCA	M.S. for SCA	M.S. for reciprocal effects	Error M.S.
D.F.	4	10	10	48
Onset-of-heading	22.7031** 39.0469**	2.1187** 4.0062**	0.4000 0.2431	0.2390 0.5096
Final heading	31.3750** 46.0000**	2.3062** 5.6812**	0.5625* 0.3375	0.2126 0.7635
Heading-span	1.3652* 1.5268	0.5275* 1.9586*	0.2319 0.4347	0.2507 0.9094
Plant height	1169.9375** 1415.1094**	17.7062** 25.2250**	47.0742** 27.7873	4.4982 39.3587
Number of tillers per plant	1.9502* 9.3584**	0.8808 1.0986	0.5834 0.4896	0.6970 1.2179
Number of spikelets per spike	3.0322** 3.2627**	0.2066 0.2785	0.2304 0.0921	0.1753 0.9593
Number of seeds per spike	64.1406** 34.2031*	3.4828 2.9781	1.6961 1.3182	2.9497 10.7170
Weight of seeds per spike	0.1579** 0.0720*	0.0063 0.0126	0.0046 0.0048	0.0096 0.0163
1000-kernel weight	41.4063** 28.2812**	2.6574 3.3535	1.5148 0.4488	2.5674 6.8000
Yield per plant	13.2227** 2.7109	1.8699 1.3242	1.8725 1.0820	1.4968 2.2172

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level

** Significant at 1% level

TABLE 35

Mean squares from the analysis of variance
of 5 x 5 F_2 diallel set for ten characters at two locations.

Source of variation	D.F.	Onset-of-heading	Final heading	Heading-span	Plant height	Number of tillers per plant	Number of spikelets per spike	Number of seeds per spike	Weight of seeds per spike	1000 kernel weight	Yield per plant
α	4	68.0938** 117.0937**	73.1250 138.1719**	4.0957 4.5820	3510.5000** 4245.5000**	5.8467 28.0713**	9.0908** 0.7852*	192.3750** 190.9219*	0.4738** 0.2159**	124.1875** 84.8125**	39.6543** 8.1191
b	10	6.3812** 12.0687**	61.2437 17.0125**	1.5824 5.8754	53.0000** 75.7000*	2.6473 3.2988	0.6227 0.8395	10.5312 68.5313	0.0188 0.0377	7.9812 10.0750	5.6172 3.9770
b_1	1	36.7496 51.6675	79.5675 82.6875	0.0208 3.7408	6.4820 10.0833	1.0448 10.2491	0.2168 1.0195	3.8458 40.0176	0.0116 0.0698	0.0029 23.5447	5.3993 1.2118
b_2	4	4.1406 4.2607*	44.9219 5.1094	0.9528 7.6094	59.7031 93.1250*	1.0060 3.9525	0.0586 0.9189	17.0752 75.6230	0.0249 0.0582	9.5039 9.9443	4.0752 1.6973
b_3	5	2.1000** 10.3750**	70.6500* 13.4250**	2.3992 4.9156	56.9000** 74.6125*	4.2852* 1.3898	1.1625 0.7453	6.6250 68.5625	0.0156 0.0149	8.3625 7.5000	6.8937* 6.3586**
c	4	2.2541 1.1625	71.7542 0.5542	0.5375 2.0292	239.1536** 141.6374**	2.8807 1.7982	0.4980 0.1374	8.5938 93.4017	0.0072 0.0091	2.2230 1.3426	6.1870 1.2746
d	6	0.4972 0.4403	56.6431 1.3181	0.8014 0.8208	75.9351** 44.5118*	0.9963 1.2493	0.8198* 0.3691	2.7512 83.4116	0.0180 0.0178	6.0919 1.3488	5.2380 4.5601
Blocks x α	8	0.6094 2.6172	35.5859 2.0547	1.2484 5.3865	22.0469 59.4609	1.7603 3.1372	0.7969 1.4517	8.4609 30.6875	0.0289 0.0298	14.6484 7.3843	3.1318 12.6904
Blocks x b	20	0.8375 1.2875	42.0594 3.4312	0.8220 3.5931	14.4500 24.2156	2.9328 2.8902	0.6846 0.5980	12.5031 67.5125	0.0395 0.0373	7.5344 9.5287	4.9916 3.4434
Blocks x b_1	2	4.4151 7.9850	17.8850 19.1850	1.7017 3.0817	30.5184 181.8318	3.0592 30.4552	1.7195 0.1034	63.1927 34.0421	0.0729 0.1419	8.1275 51.5334	5.6767 10.2759
Blocks x b_2	8	1.2827 1.0347	23.4004 4.0889	1.2711 5.8386	22.0747 18.0625	5.5184 2.8100	0.8450 0.9053	15.7554 53.9883	0.0651 0.0589	11.1401 10.5664	9.3918 6.4728
Blocks x b_3	10	0.1875 0.9437	63.5938 1.6625	0.4566 2.2068	8.3312 16.0437	1.1415 0.4828	0.5141 0.4555	6.0937 88.4437	0.0196 0.0133	5.3578 5.4691	1.8984 0.6773
Blocks x c	8	0.9041 0.7812	71.3666 0.8979	0.4500 1.4104	9.2411 3.1023	1.2472 1.5910	0.2572 0.4212	4.8894 60.4627	0.0130 0.0084	3.9115 1.1626	3.0324 2.6685
Blocks x d	12	0.4597 1.6944	57.7347 1.5056	0.5056 0.4000	9.1118 11.1003	1.4759 1.2712	0.2664 0.7791	5.7155 94.8401	0.0207 0.0262	5.9257 3.7547	5.5405 3.2056
Error	48	0.7161 1.5265	49.7838 2.2982	0.7520 2.7299	13.5133 23.2919	2.0922 2.5101	0.5275 0.7561	8.8636 67.0319	0.0286 0.0285	7.7141 6.3335	4.4923 4.7959

*Significant at 5% level

**Significant at 1% level

First reading under each column refers to Ellerslie and second to Parkland. Error D.F. comprises of block interaction with D.F. of ($\alpha+b+c+d$). Each component has been tested against its own block interaction.

TABLE 36

Analysis of variance of $W_p - V_p$
from F₂ diallel set for ten characters at two locations.

Character	Block M.S.	Entry M.S.	Error M.S.
Onset-of-heading	7.3843 8.3904	0.2675 2.4463	0.4078 0.8015
Final heading	2.3424 35.5057	0.7644 5.2120	0.2218 3.7671
Heading-span	0.0046 8.1741	0.1472 4.4720	0.2028 2.0416
Plant height	10448.0312 4912.7812	150.1719 427.7812**	157.5547 38.5703
Number of tillers per plant	1.2452 0.8319	2.4152* 0.5920	0.5435 2.3435
Number of spikelets per spike	0.9966 0.0373	0.0884 0.1622	0.0807 0.0598
Number of seeds per spike	636.7512 188.8423	26.2899 15.5951	19.7865 6.5623
Weight of seeds per spike	0.0089 0.0025	0.0002 0.0004	0.0003 0.0003
1000-kernel weight	313.4819 2.8203	7.3413 11.5522	1.9490 18.5395
Yield per plant	61.8167 12.4054	9.5905 2.6444	3.0673 2.7121

First reading under each column refers to Ellerslie and second to Parkland.

* Significant at 5% level

**Significant at 1% level

TABLE 37

Estimates of second degree statistics parameters
for ten characters from F₂ diallel set at two locations.

Character	V_{OLO}	W_{OLO2}	V_{OL2}	V_{VL2}	$(M_{L1} - M_{LO})^2$
Onset-of-heading	15.0000 15.7002	5.8158 7.6168	2.2734 30.9072	3.3381 5.9146	1.9600 2.7759
Final heading	16.9668 27.1514	7.2016 11.1402	3.1475 4.6084	4.3006 7.4500	1.5891 4.4100
Heading-span	0.5889 3.6100	0.2362 0.6751	0.1367 0.1528	0.4003 1.1320	0.0011 0.1995
Plant height	486.7784 518.4434	235.7205 226.4807	117.0059 141.5420	125.8615 154.1387	0.3456 0.5377
Number of tillers per plant	1.4343 5.4749	0.5030 2.1069	0.1948 0.9358	0.6359 1.4856	0.0557 0.5465
Number of spikelets per spike	1.2283 0.5749	0.6072 0.4241	0.3030 0.3264	0.4072 0.4663	0.0115 0.0543
Number of seeds per spike	28.9980 12.2275	12.8064 5.6326	6.4111 3.4180	8.1627 4.9113	0.2050 0.2733
Weight of seeds per spike	0.0384 0.0360	0.0241 0.0133	0.0158 0.0072	0.0189 0.0135	0.0006 0.0037
1000-kernel weight	16.7744 13.1670	7.8586 5.6221	4.1396 2.8271	5.4666 4.5039	0.6001 1.2557
Yield per plant	5.4558 0.8875	2.4823 0.4078	1.3221 0.2711	2.2580 0.9338	0.4412 0.0646

First reading under each column refers to Ellerslie and the second to Parkland.

additive gene effects, is relatively more important than SCA, which is due to non-additive gene effects, as far as selection on the basis of these characters is concerned. (3) The significance of SCA variances implies that hybrids yield much less than would be expected on the basis of the GCA's of their parents. This suggests that character instability of a hybrid is largely due to high SCA variances associated with its parents.

Diallel cross analysis

The results of the analysis of variance performed after Hayman (1954a) on the F_2 diallel table are given in Table 35. The presence of additive gene effects is shown by significant a 's for onset-of-heading, plant height, number of spikelets per spike, number of seeds per spike, weight of seeds per spike and 1000-kernel weight at both locations; also for yield per plant at Ellerslie and final heading and number of tillers per plant at Parkland. Significant additive gene effects for these characters suggest substantial differences among the parental lines used. Significant b 's for onset-of-heading, final heading and plant height shows that dominance is present while significant b_2 's indicate some asymmetry of loci exhibiting dominance for these characters, suggesting that some parents contain more dominant alleles than others. Significant b_3 's for onset-of-heading, final heading, plant height and yield per plant at both locations, and for number of tillers per plant at Ellerslie, imply that specific combining ability for these characters is comparatively more important than general combining ability when a pedigree selection procedure is followed in a breeding programme (Mather and Jinks, 1971).

TABLE 38

Estimates of genetic components of variation and their standard errors
from F₂ diallel set for ten characters at two locations.

Character	D	F	H ₁	H ₂	h ²	E
Onset-of-heading	14.6708 ± 0.2067** 15.1911 ± 0.6740**	6.4497 ± 0.5162** 0.3223 ± 1.6836	4.4673 ± 0.5581** 7.5679 ± 1.8202**	3.7803 ± 0.5062** 7.0114 ± 1.6509**	7.6875 ± 0.3418** 10.6973 ± 1.1146**	0.2391 ± 0.0844** 0.5091 ± 0.2752
Final heading	16.7506 ± 0.3746** 28.3875 ± 0.5310**	4.8680 ± 0.9356** 8.8251 ± 1.3263**	4.8009 ± 1.0115** 10.4043 ± 1.4339**	4.1802 ± 0.9175** 9.8386 ± 1.3006**	6.2127 ± 0.6194** 17.1511 ± 0.8781**	0.2161 ± 0.1529 0.7639 ± 0.2186**
Heading-span	0.3383 ± 0.1606* 2.7012 ± 0.7337**	-0.0677 ± 0.4012 3.4300 ± 1.8327	0.5938 ± 0.4337 3.0730 ± 1.9814	0.5534 ± 0.3934 2.0971 ± 1.7971	-0.1560 ± 0.2656 0.2157 ± 1.2133	0.2407 ± 0.0656** 0.9100 ± 0.2995**
Plant height	482.2761 ± 5.3403** 510.7024 ± 11.4837**	25.2691 ± 13.3401 -38.3252 ± 28.6862	35.6431 ± 14.4221** 48.9489 ± 31.0130	26.4261 ± 13.0810* 34.9049 ± 28.1292	-1.4962 ± 8.8316 -2.8030 ± 18.9913	4.4983 ± 2.1802* 7.7409 ± 4.6882
Number of tillers per plant	0.7373 ± 0.1694** 4.7055 ± 0.1993**	0.0199 ± 0.4232 1.5989 ± 0.4978**	0.1536 ± 0.4575 0.9894 ± 0.5362	0.3705 ± 0.4150 0.6605 ± 0.4831	-0.2232 ± 0.2802 1.6941 ± 0.3296**	0.6970 ± 0.0692** 0.7694 ± 0.0814**
Number of spikelets per spike	1.0529 ± 0.0515** 0.3233 ± 0.1134**	-0.1827 ± 0.1287 -0.8483 ± 0.2834**	-0.0278 ± 0.1391 0.0896 ± 0.3064	0.0658 ± 0.1262 0.0562 ± 0.2779	-0.0660 ± 0.0852 0.0565 ± 0.1876	0.1753 ± 0.0210** 0.2516 ± 0.0463**
Number of seeds per spike	26.0475 ± 1.1122** 8.7961 ± 1.0111**	3.2297 ± 2.7783 -2.1931 ± 2.5257	2.7517 ± 3.0037 0.4207 ± 2.7306	1.1052 ± 2.7244 -0.8894 ± 2.4767	-1.0681 ± 1.8394 -1.0827 ± 1.6721	2.9505 ± 0.4541** 0.0095 ± 0.0021**
Weight of seeds per spike	0.0288 ± 0.0019** 0.0266 ± 0.0052**	-0.0313 ± 0.0047** 0.0075 ± 0.0130	-0.0073 ± 0.0050 0.0121 ± 0.0140	-0.0065 ± 0.0046 0.0062 ± 0.0127	-0.0036 ± 0.0031 0.0088 ± 0.0086	0.0095 ± 0.0008** 0.0095 ± 0.0021**
1000-kernel weight	14.2071 ± 0.8036** 11.0585 ± 1.3289**	-0.9663 ± 2.0075 1.3155 ± 3.3195	0.5315 ± 2.1703 3.2122 ± 3.5888	0.1733 ± 1.9685 2.4900 ± 3.2551	1.6424 ± 1.3290 3.6732 ± 2.1976	2.5673 ± 0.3281** 2.1085 ± 0.5425**
Yield per plant	3.9588 ± 0.7287** -0.7108 ± 0.3318*	-0.8142 ± 1.8203 -1.7740 ± 0.8287*	0.6660 ± 1.9679 -1.1636 ± 0.8960	0.7492 ± 1.7849 -0.5453 ± 0.8126	0.1937 ± 1.2051 -0.7644 ± 0.5487	1.4970 ± 0.2975** 1.5982 ± 0.1354**

First reading under each column refers to Ellerslie and second to Parkland.

* Significant at 5% level

**Significant at 1% level

TABLE 39

Proportional estimates of genetic parameters
for ten characters from F_2 diallel set at two locations.

Character	$[H_1/D]^{1/2}$	$[H_2/4H_1]$	$\left[\frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F} \right]$	$r [Y_r/W_r + V_r]$	$\left \frac{h^2}{H} \right $	[Heritability]
Onset-of-heading	0.5501* 0.7058*	0.2116* 0.2316*	2.3175* 1.0305†	0.9658 0.8792	2.0336* 1.5257*	1.0751 0.6206
Final heading	0.5354* 0.6279*	0.2177* 0.2364*	1.7451* 1.7279*	0.9906 0.9550	1.4862* 1.7432*	0.9545 0.8596
Heading-span	1.3249 1.0666	0.2330 0.1706	0.8596 3.9415	0.9362 0.2426	-0.2818 0.1028	0.1689 0.4513
Plant height	0.2719* 0.3096	0.1854* 0.1783	1.2131† 0.7838	0.7522 0.0827	-0.0566 -0.0803	0.9443 0.8120
Number of tillers per plant	0.4565 0.4585	0.6029 0.1669	1.0610 2.1772	-0.1501 0.9489	-0.6023 2.5648	0.2015 0.6559
Number of spikelets per spike	0.1626 0.5264	-0.5913 0.1569	0.3040 -0.4273	0.8604 -0.1745	-1.0027 1.0043	0.5515 0.1425
Number of seeds per spike	0.3250 0.2187	0.1004 -0.5285	1.4714 0.2739	0.0765 -0.1187	-0.9664 1.2174	0.6969 0.7683
Weight of seeds per spike	0.5034 0.6752	0.2241 0.1272	-0.0379 1.5290	-0.2629 -0.3126	0.5555 1.4330	0.3171 0.3843
1000-kernel weight	0.1934 0.5390	0.0815 0.1938	0.7009 1.2481	-0.5825 -0.8244	-9.4800 1.4752	0.5469 0.5170
Yield per plant	0.4102 1.2795	0.2812 0.1172	0.5991 0.0125	0.1919 -0.4069	0.2585 1.4016	0.3464 -0.1129

First reading under each column refers to Ellerslie and second to Parkland.

*Genetic components of variation for the characters significantly different from zero at $P \leq 0.05$

†Components D and H_1 significant, F non-significant ($P > 0.05$).

In regard to the testing of the assumptions underlying the analysis, significant c 's for plant height at each of the two locations indicate that there are reciprocal differences for this character. The results of a test of other assumptions, by the analysis of variance of $W_r - V_r$ differences are given in Table 36. Except for plant height at Parkland and number of tillers per plant at Ellerslie, the $W_r - V_r$ differences were homogeneous and therefore these other assumptions were generally not invalidated by the data. Two exceptions (for plant height and number of tillers per plant) will be considered later.

Estimates of second degree statistics and components of genetic variation derived from the analysis of F_2 diallel table after replacement of off-the-diagonal cells with their corresponding common means, are given in Tables 37 and 38. In Table 38, component significances are tested with 25 D.F. (35 statistics provided by Table 37, with 10 constants fitted to them). Proportional values of the genetic parameters calculated from Table 38 are given in Table 39, which shows the over-all genetic situation with regard to the inheritance of each character. The results of Tables 38 and 39 together with W_r, V_r graphs and standardized deviation graphs of Y_r and $(W_r + V_r)$ are discussed under each character.

All components of variation for onset-of-heading (Table 38) except F and E at Parkland were significant. The mean degree of dominance (0.55 at Ellerslie and 0.75 at Parkland) indicates that the character is partially dominant at both locations. This is also shown by the regression line in the W_r, V_r graph (Figure 21) which intersects the limiting parabola

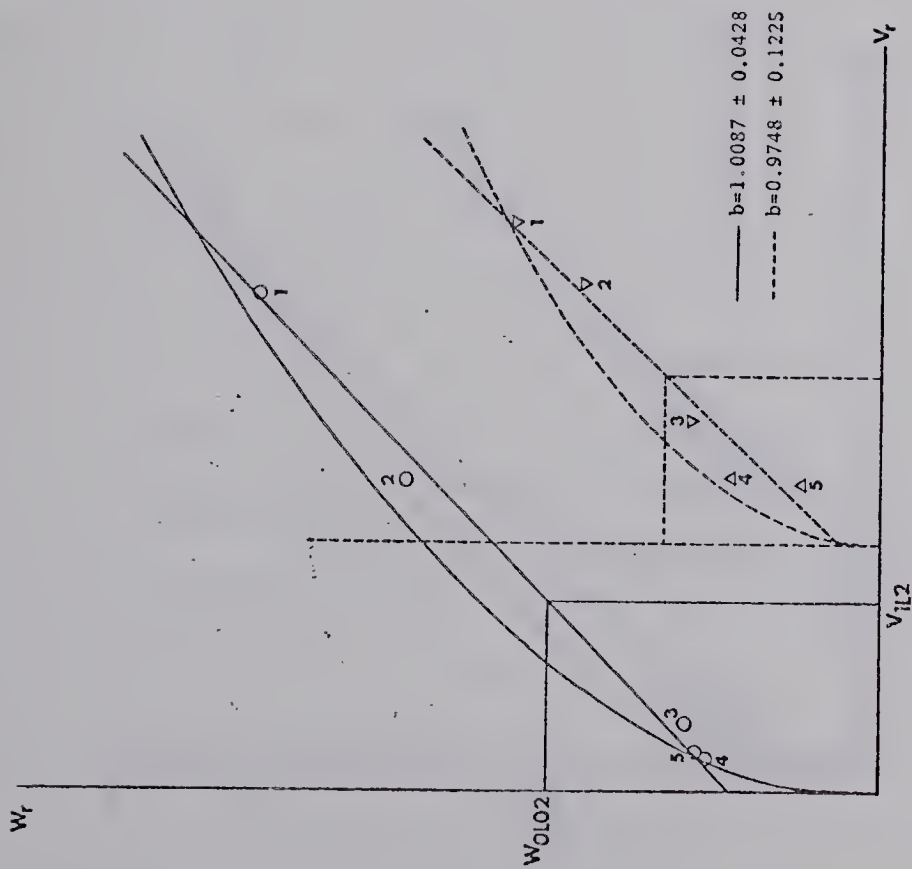


Figure 21. W_r , V_r graph for onset-of-heading from F_2 diallel set.

— $\circ = W_r$, V_r intercepts at Ellerslie
 --- $\Delta = W_r$, V_r intercepts at Parkland

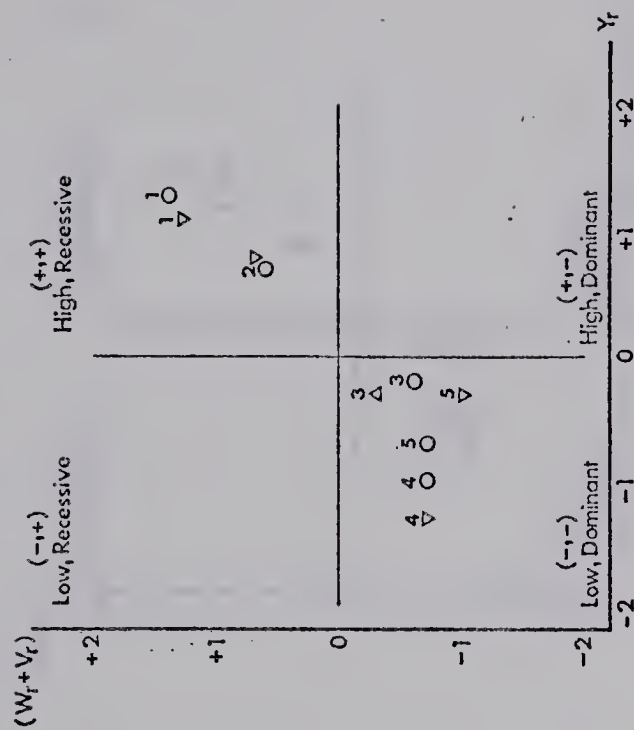


Figure 22. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for onset-of-heading from F_2 diallel set.

$\circ = Y_r$, $[W_r + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r$, $[W_r + V_r]$ intercepts at Parkland

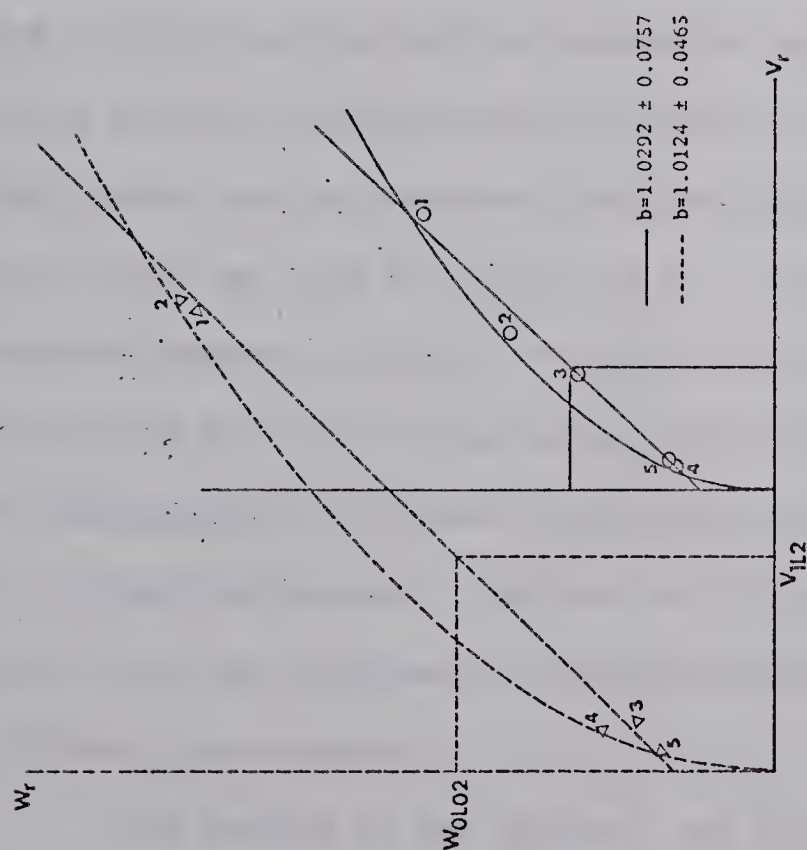


Figure 23. W_r, V_r graph for final heading from F_2 diallel set.

— $0 = W_r$ V_r intercepts at Ellerslie
 --- $\Delta = W_r$ V_r intercepts at Parkland

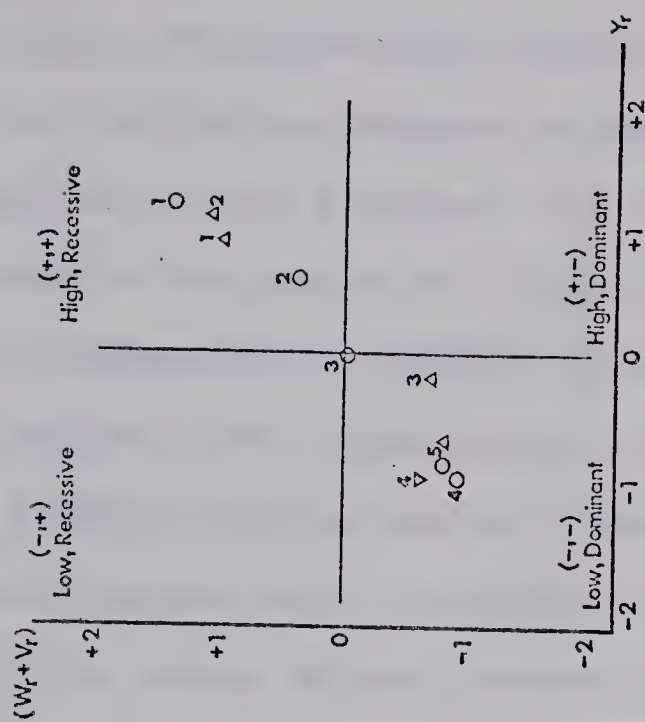


Figure 24. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for final heading from F_2 diallel set.

$$\begin{aligned} 0 &= Y_r, \quad [W_r + V_r] \text{ intercepts at Ellerslie} \\ \Delta &= Y_r, \quad [W_r + V_r] \text{ intercepts at Parkland} \end{aligned}$$

above the origin. The proportion of positive to negative alleles in the parents at loci exhibiting dominance is approximately 0.25, indicating equal proportions at both locations. The proportion of dominant to recessive genes in the parents is 2.3 and 1.03 for Ellerslie and Parkland, suggesting a preponderance of dominant genes in the parents. Figure 21 shows that Marquis is the highly recessive parent at both locations, as it lies farthest from the point of origin of the regression line. Ciano at Ellerslie and Inia at Parkland rank as the two most dominant parents because of their nearness to the point of origin of the regression line. The coefficient of correlation between parental order of dominance and parental measurements is 0.96 at Ellerslie and 0.87 at Parkland suggesting that most of the negative genes (for early maturing) are dominant. The distribution of parents with respect to order of dominance is shown in standardized deviation graph of Figure 22. Marquis and Chinook at both locations fall into the (+,+) quadrant indicating that they contain mostly recessive genes responsible for lateness while Khush-hal, Ciano and Inia fall into the (-,-) quadrant and are therefore early heading dominant parents. The number of groups of genes controlling onset-of-heading has been estimated as 2.03 for Ellerslie and 1.52 for Parkland indicating that at least two groups of genes exhibiting dominance control the onset-of-heading. The heritability estimates of 107.51% and 62.06% show that the character is highly heritable but with low stability under different environments.

The results of the analysis for final heading (Tables 38, 39; Figures 23, 24) and heading-span (Tables 38, 39; Figures 25, 26) are subject

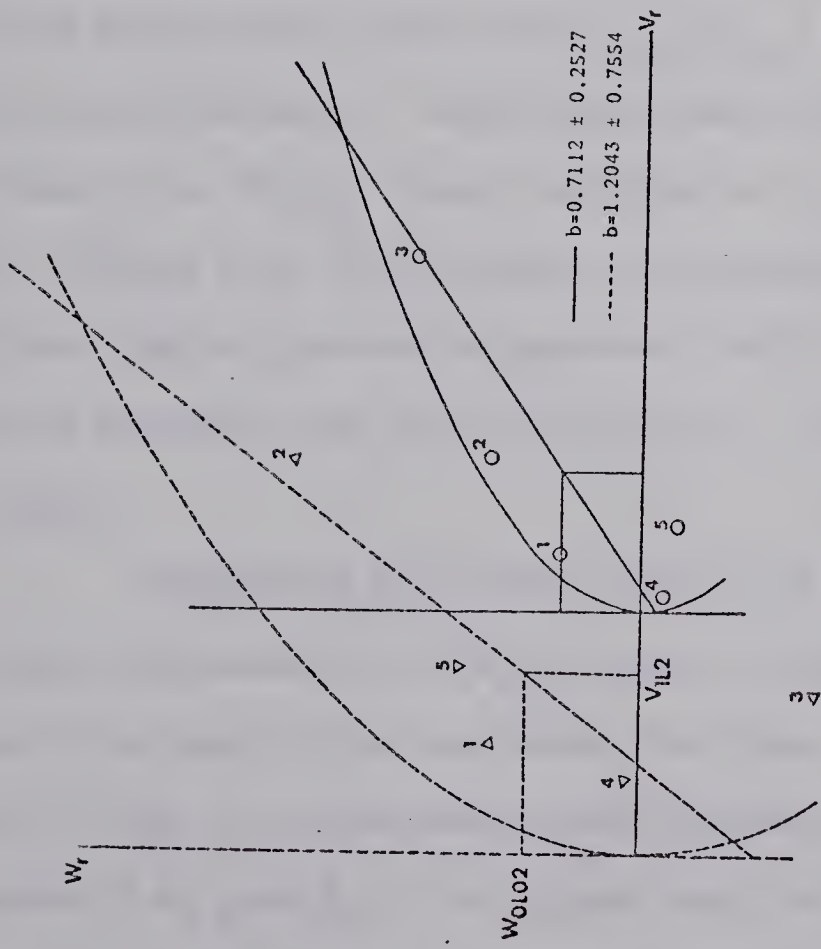


Figure 25. W_r, V_r graph for heading-span from F_2 diallel set.

— $o = W_r, V_r$ intercepts at Ellerslie
 --- $\Delta = W_r, V_r$ intercepts at Parkland

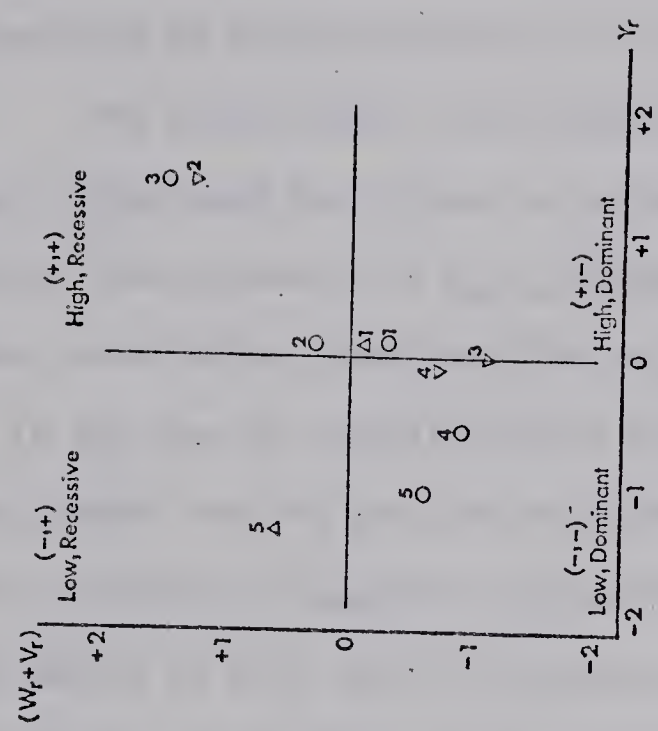


Figure 26. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for heading-span from F_2 diallel set.

$o = Y_r, [W_r + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r, [W_r + V_r]$ intercepts at Parkland

to the same kind of interpretations as for onset-of-heading.

For plant height, the components of variation, D , H_1 , H_2 and E were significant for Ellerslie but none except D were significant at Parkland. Heterogeneity of W_r - V_r values (Table 36) implies either non-allelic interaction, multiple allelism or correlated gene distribution. In the case of correlated gene distribution, the W_r, V_r curve is convex upwards and the mean degree of dominance is seriously inflated, giving an impression of apparent over-dominance (Hayman, 1954b) in a situation where, in fact, partial dominance exists. In the case of multiple allelism, the effects are extremely complicated. Models to explain the consequences in terms of W_r, V_r graphs, are pending. It might show spurious dominance (Hayman, 1954b) by scattering the W_r, V_r points and thus causing their mean (V_{1L2}, W_{0L02}) to lie inside, and not on the limiting parabola. Non-allelic interaction of the complementary type distorts the (W_r, V_r) graph, inflates the $(H_1 \div D)^{1/2}$ and depresses (h^2/H_2) , but has very little effect on the estimator of gene frequency. A duplicate type of interaction depresses (h^2/H_2) by increasing the proportion of dominants, but does not alter $(H_1 \div D)^{1/2}$, $H_2/4H_1$ and the W_r, V_r graph.

Considering the various effects of the three above-mentioned conditions, and examining the W_r, V_r graph for plant height at Parkland (Figure 27) we come to the conclusion that there is actually no non-validity of any of the above-mentioned hypotheses. This is because the regression of W_r upon V_r is not significantly different from one, the array W_r, V_r intercepts do not show any convexity upwards or downwards

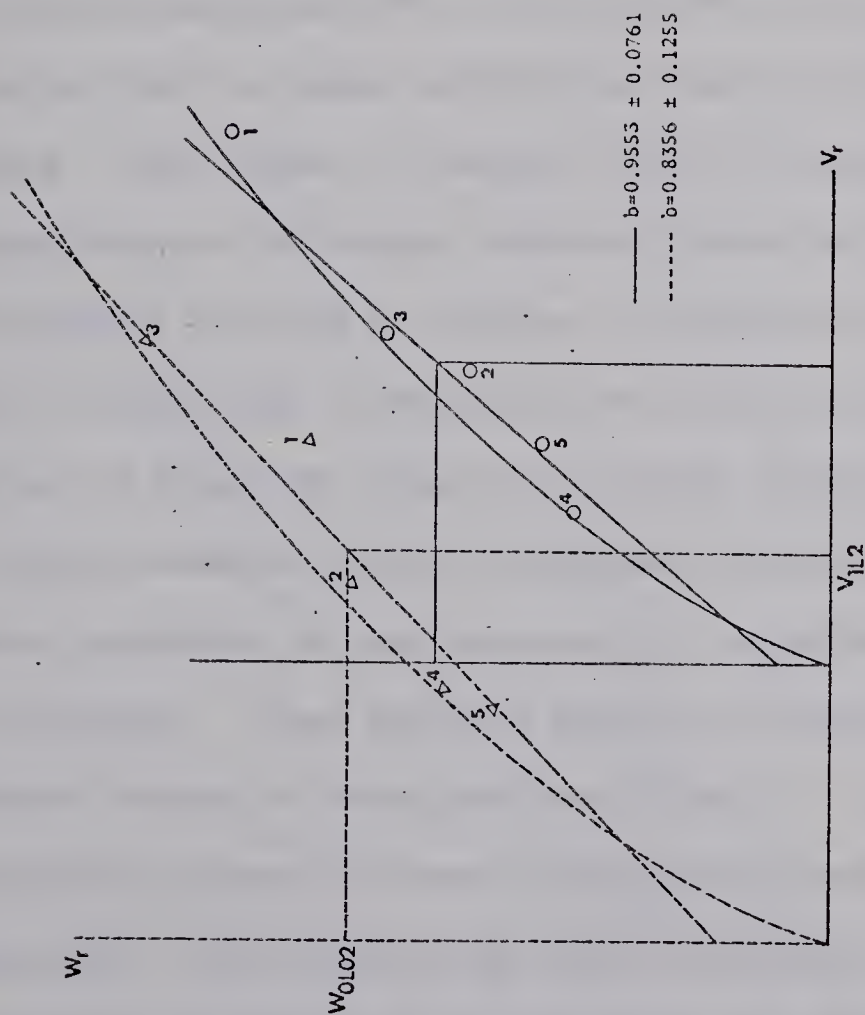


Figure 27. W_r , V_r graph for plant height from F_2 diallel set.

— $0 = W_r$, V_r intercepts at Ellerslie
 --- $\Delta = W_r$, V_r intercepts at Parkland

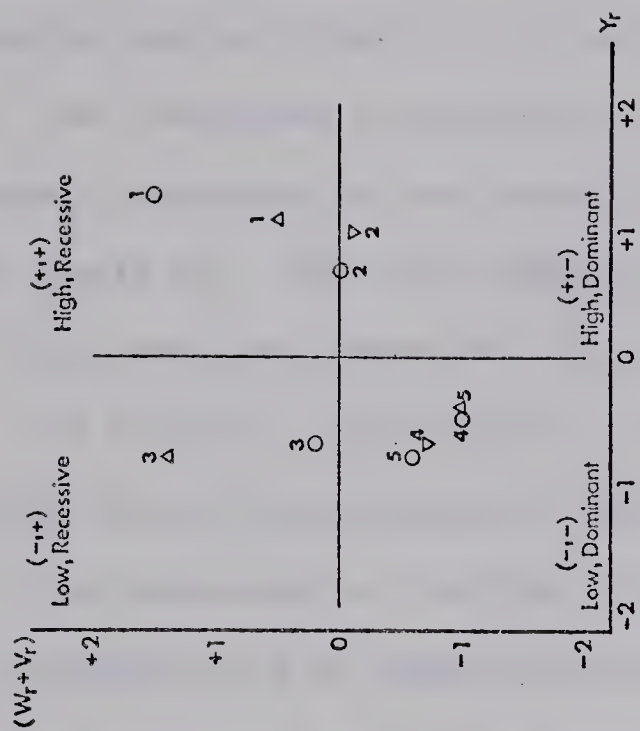


Figure 28. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for plant height from F_2 diallel set.

$o = Y_r$, $[W_r + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r$, $[W_r + V_r]$ intercepts at Parkland

and there are no serious effects on the estimates of genetic parameters (Table 39). Our conclusion is supported by the fact that all the estimates of genetic components of variation at Parkland except D are non-significant (Table 38). The only reason we might give for the heterogeneity of $W_r - V_r$ over the arrays is a strong environmental effect.

At Ellerslie, plant height is inherited as a partially dominant trait since the mean degree of dominance is 0.27 (See also Figure 27). The proportion of positive to negative alleles at loci exhibiting dominance is 0.18 indicating asymmetry, while the proportion of dominant to recessive genes in the parents is 1.2 (close to equality). The coefficient of correlation between the parental order of dominance and parental measurements is 0.75 at Ellerslie and 0.08 at Parkland, indicating that the genes contributing towards shortness are mostly dominant. With respect to parental order of dominance (Figure 27 and 28) Marquis rates as the highly recessive parent for tallness at Ellerslie and Khush-hal likewise at Parkland. Ciano ranks as the most dominant parent for shortness at Ellerslie and similarly Inia at Parkland. Examination of Figure 28 reveals that though Marquis and Khush-hal rank as the highly recessive parents, Khush-hal nevertheless contributes towards reduced expression of the character (-,+ quadrant) as compared to Marquis (+,+ quadrant). Ciano and Inia rank as the most dominant parents for shortness because of their position in the (-,-) quadrant. Chinook, contributing towards tallness, has recessive and dominant genes in equal proportions. The character has high heritability (94.43% at Ellerslie and 81.20% at Parkland) and thus seems to be little affected by environmental conditions.

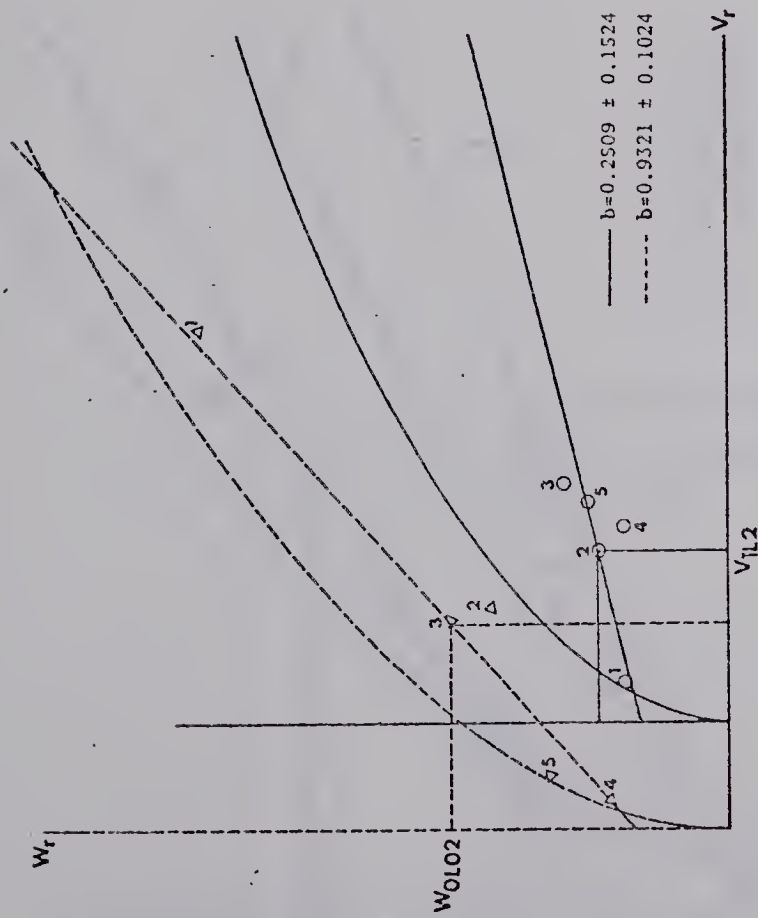


Figure 29. W_r , V_r graph for number of tillers per plant from F_2 diallel set.

— $o = W_r$, V_r intercepts at Ellerslie
 --- $\Delta = W_r$, V_r intercepts at Parkland

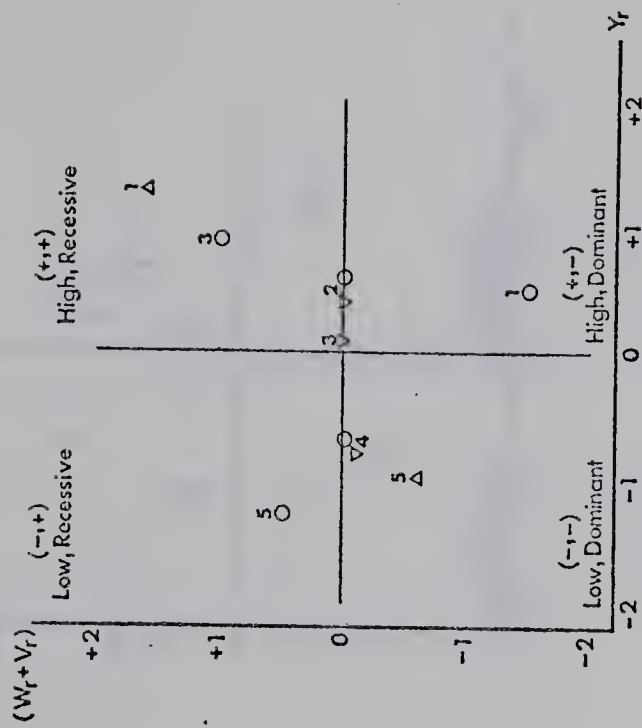


Figure 30. Standard deviation graph

of $[Y_r]$ and $[W_r + V_r]$ for number of tillers per plant from F_2 diallel set.

$o = Y_r$, $[W_r + V_r]$ intercepts at Ellerslie

$\Delta = Y_r$, $[W_r + V_r]$ intercepts at Parkland

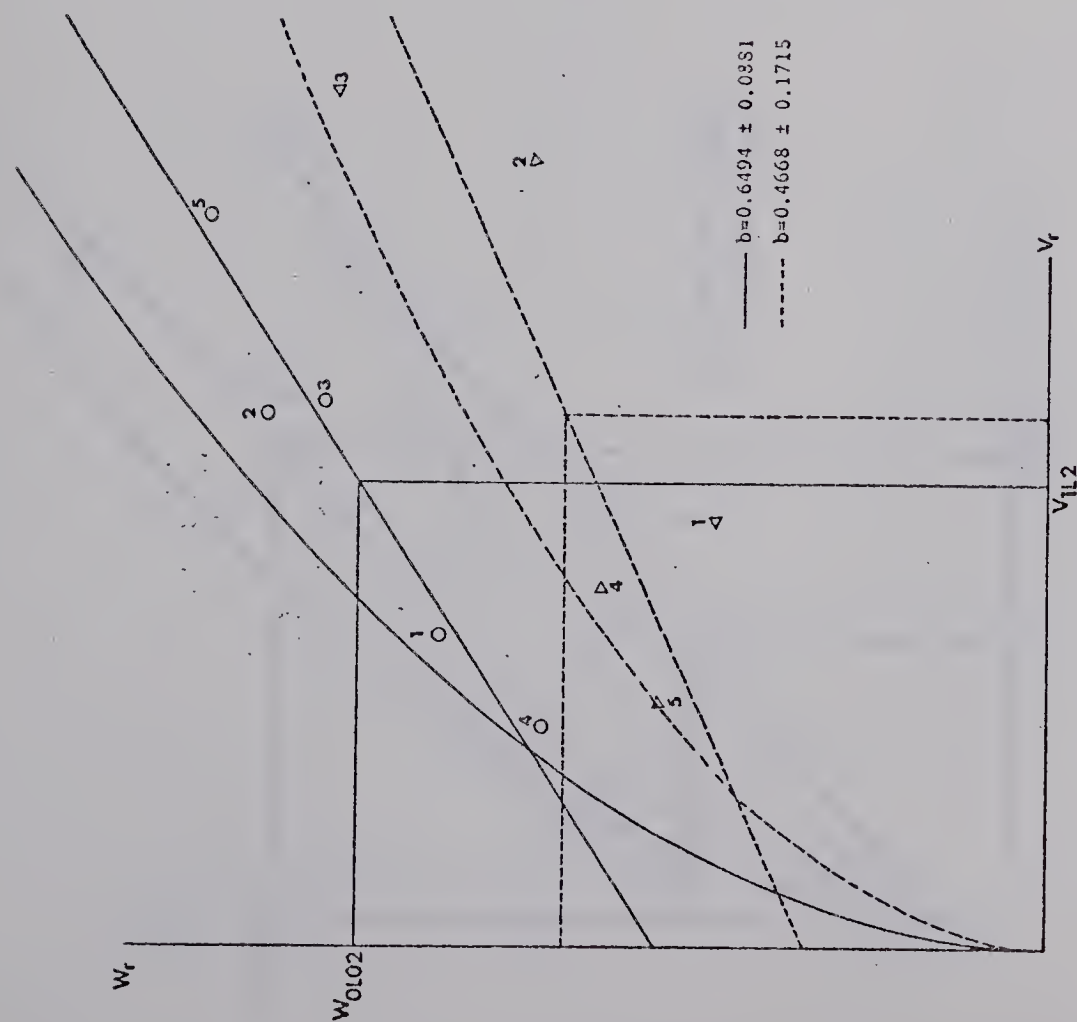


Figure 31. W_r , V_r graph for number of spikelets per spike from F_2 diallel set.

— $o = W_r$, V_r intercepts at Ellerslie

--- $\Delta = W_r$, V_r intercepts at Parkland

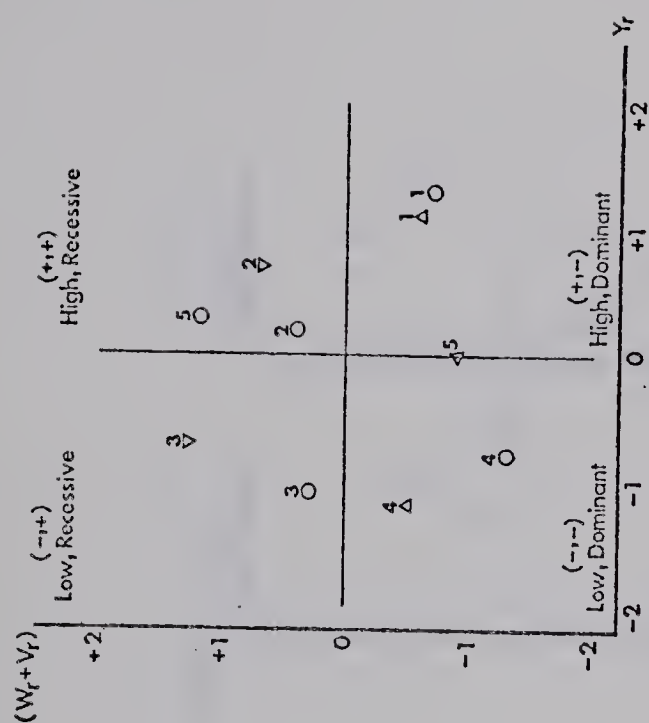


Figure 32. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of spikelets per spike from F_2 diallel set.

$o = Y_r$, $[W_r + V_r]$ intercepts at Ellerslie

$\Delta = Y_r$, $[W_r + V_r]$ intercepts at Parkland

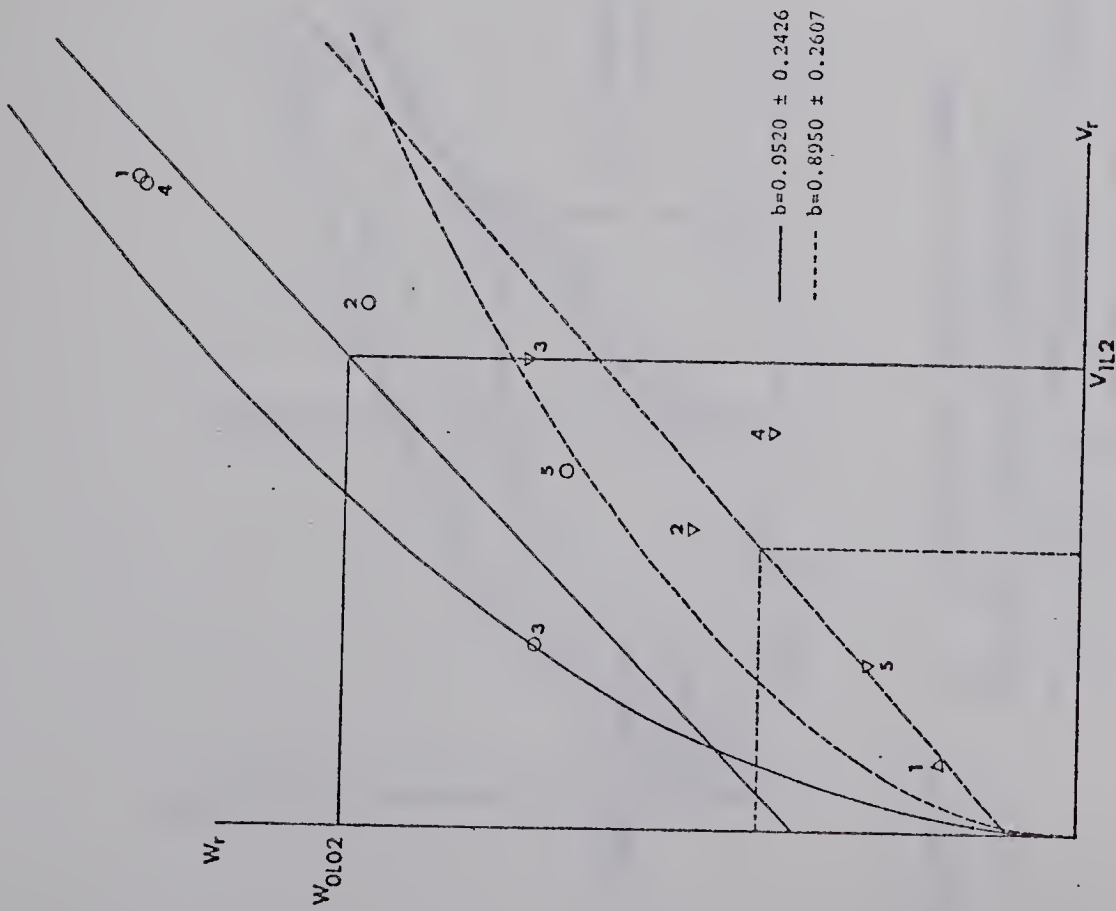


Figure 33. W_r, V_r graph for number of seeds per spike from F_2 diallel set.

— $o = W_r, V_r$ intercepts at Ellerslie
 - - - $\Delta = W_r, V_r$ intercepts at Parkland

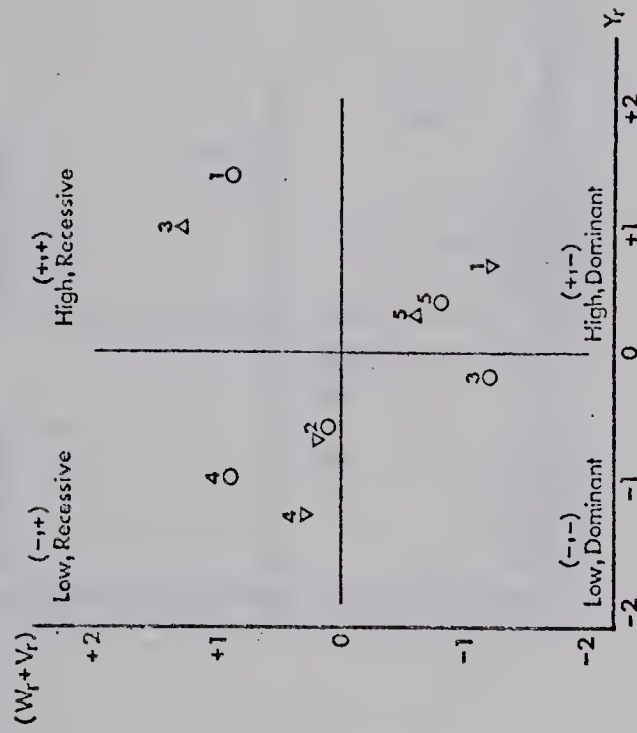


Figure 34. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of seeds per spike from F_2 diallel set.

$o = Y_r, [W_r + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r, [W_r + V_r]$ intercepts at Parkland

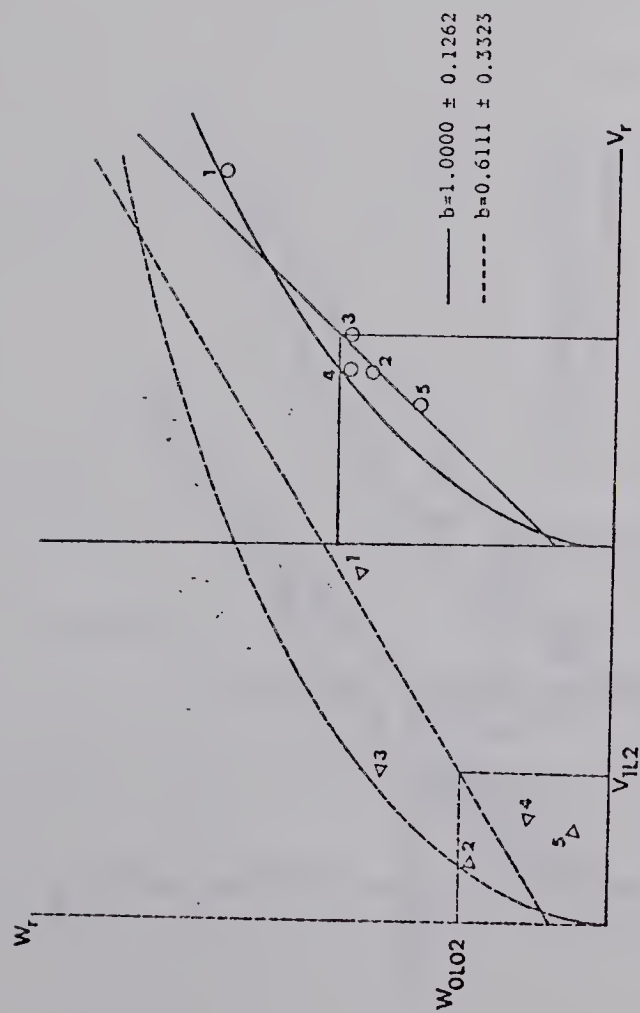


Figure 35. W_r, V_r graph for weight of seeds per spike from F_2 diallel set.

— $o = W_r, V_r$ intercepts at Ellerslie
 --- $\Delta = W_r, V_r$ intercepts at Parkland

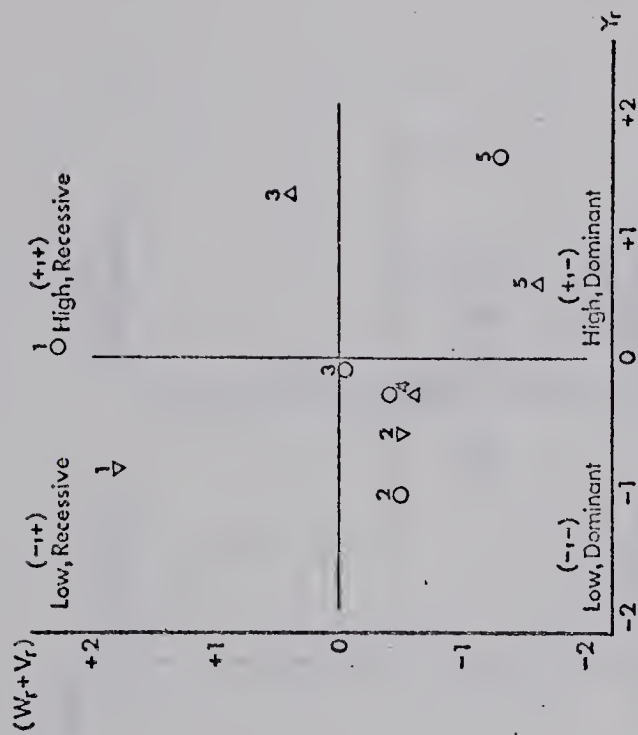


Figure 36. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for weight of seeds per spike from F_2 diallel set.

$o = Y_r, [W_r + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r, [W_r + V_r]$ intercepts at Parkland

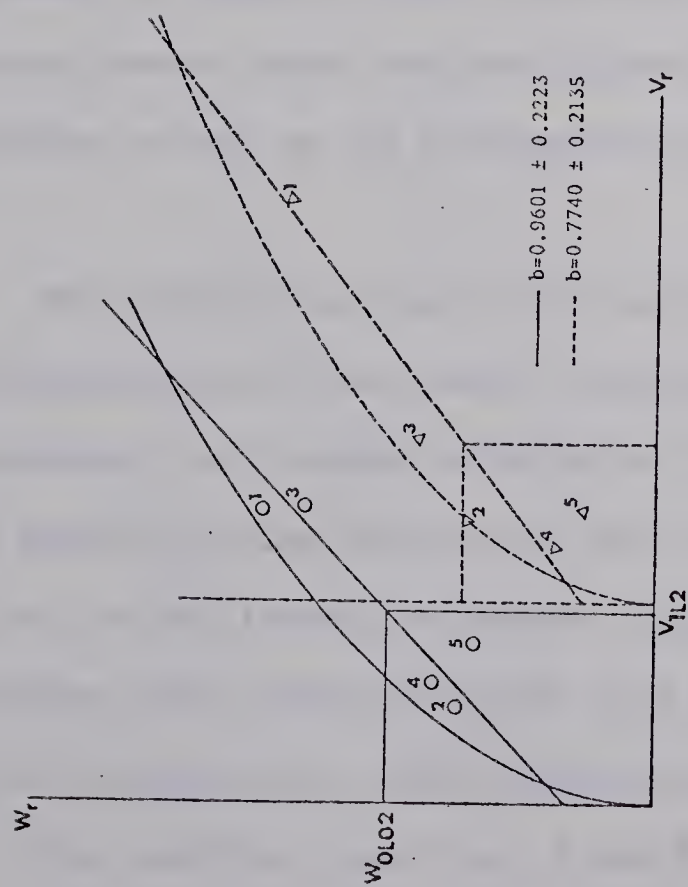


Figure 37. W_r , V_r graph for 1000-kernel weight from F_2 diallel set.

— $\circ = W_r$, V_r intercepts
at Ellerslie
--- $\Delta = W_r$, V_r intercepts
at Parkland

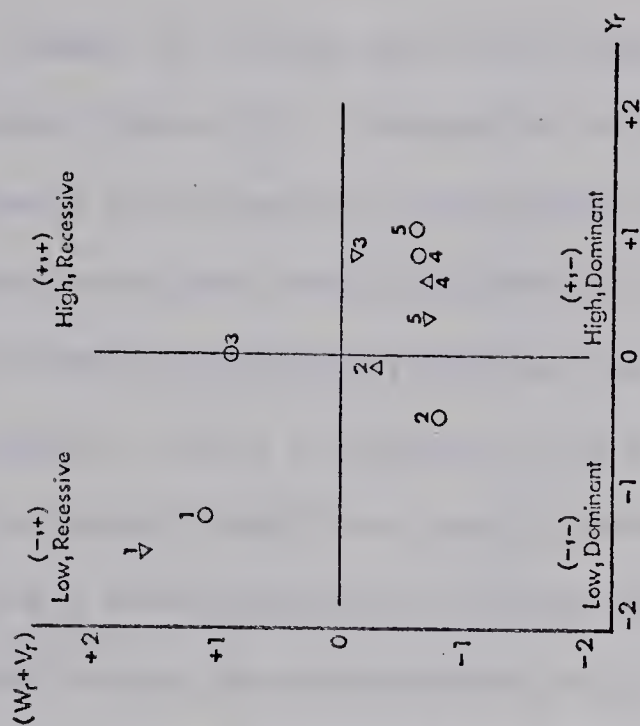


Figure 38. Standardized deviation graph

of $[Y_r]$ and $[W_r + V_r]$ for 1000-kernel weight from F_2 diallel set.

$\circ = Y_r$, $[W_r + V_r]$ intercepts
at Ellerslie

$\Delta = Y_r$, $[W_r + V_r]$ intercepts
at Parkland

Number of tillers per plant showed heterogeneity of $W_r - V_r$ values (Table 36). Examination of the W_r, V_r graph (Figure 29) and a review of the effects of non-allelic gene interaction, multipleallelism and correlated gene distribution upon the analysis, reveals that none of these conditions invalidate the corresponding null hypotheses. Moreover, since at Ellerslie the environmental component of variation is highly significant and all other components of genetic variation but D non-significant, the environmental variation is the most probable reason for heterogeneity of $W_r - V_r$ values. Since the ratios (Table 39) expressing the mean degree of dominance, the proportion of alleles with positive and negative effects at loci exhibiting dominance, the proportion of dominant and recessive genes in the parents and the number of groups of genes controlling the character were based on parameters some of which were not significant (Table 38) their interpretation as well as the interpretation of the graphs is of little value.

The general features of the diallel analysis with respect to the interpretation of the results from Tables 38 and 39 for other yield components, viz., number of spikelets per spike (Figures 31, 32), number of seeds per spike (Figures 33, 34), weight of seeds per spike (Figures 35, 36) and 1000-kernel weight (Figures 37, 38) are the same. The conclusions drawn therefrom differ with respect to the relative position of the parents for their ranking order of dominance.

For yield per plant, only D and E components of variation

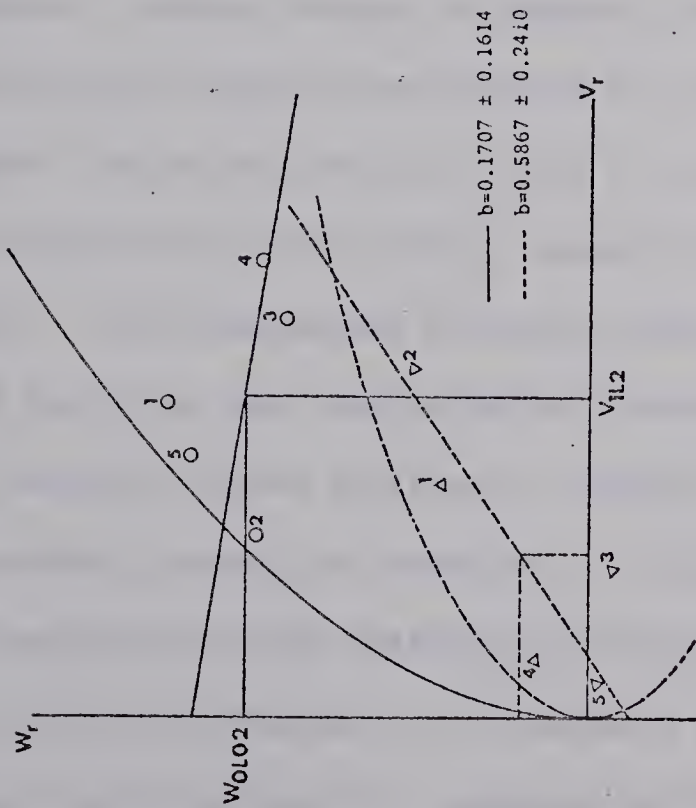


Figure 39. W_r, V_r graph for yield per plant from F_2 diallel set.

— $O = W_r, V_r$ intercepts
at Ellerslie
--- $\Delta = W_r, V_r$ intercepts
at Parkland

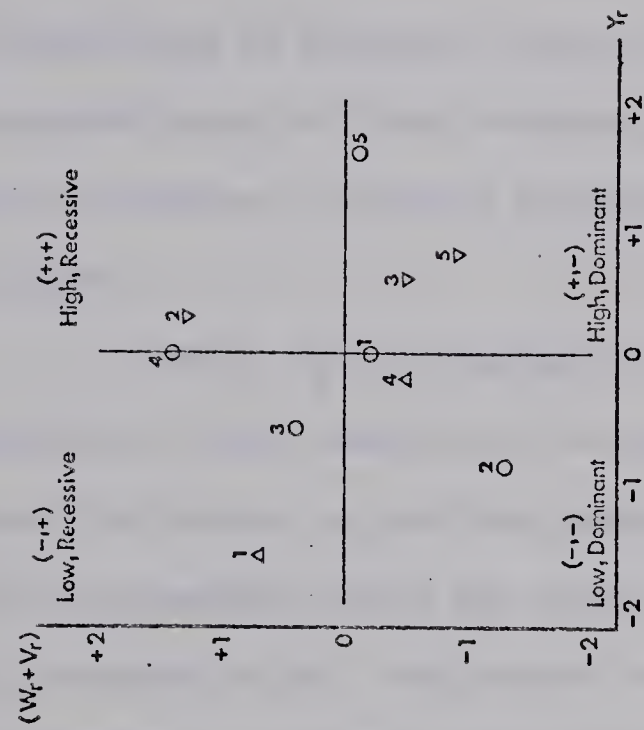


Figure 40. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for yield per plant from F_2 diallel set.

$O = Y_r, [W_r + V_r]$ intercepts
at Ellerslie
 $\Delta = Y_r, [W_r + V_r]$ intercepts
at Parkland

were significant at Ellerslie while D , F and E at Parkland. Because of non-significance of other components of variation, the interpretation of estimates of genetic parameters given in Table 39 would be meaningless.

The W_r , V_r and standardized deviation graphs are interesting in their absurdity. The location effect on yield is sufficiently drastic so that the regression line, though cutting the limiting parabola above its origin (apparent partial dominance) shows a negative slope. The latter (at Ellerslie) implies that for every increase in variance of the r th array, there is a proportional decrease in parent-offspring covariance of that array. The regression line, in this case, cuts the limiting parabola in such a way that the recessive and dominant W_r , V_r array intercepts are difficult to define. However Figure 39 suggests that Ciano may be regarded as the highly recessive and Chinook the most dominant parent. At Parkland, the regression of W_r upon V_r reveals over-dominance. Chinook may be classified as the highly recessive and Inia the most dominant parents. The standardized deviation graph of Figure 40 reveals that, except for Inia, the ranking order for dominance of the parents seems to be altered between locations. Marquis, the recessive parent, with low yielding capacity at Parkland (-,+ quadrant) becomes dominant and comparatively high yielding at Ellerslie (+,- quadrant). Chinook, low yielding and dominant (-,- quadrant) at Ellerslie, becomes recessive and high yielding (+,+ quadrant) at Parkland. A similar

situation exists with Ciano. The coefficient of correlation between the parental order of dominance and parental measurements is 0.19 at Ellerslie and -0.40 at Parkland. A positive but weak correlation at Ellerslie suggests however, that genes responsible for low yielding are mostly dominant, while the comparatively high negative correlation at Parkland indicates that the genes contributing toward increased yielding are mostly dominant. The estimates of heritability seem to be questionable because of the non-significance of relative components of genetic variation.

ANALYSIS OF BACKCROSS DATA

The expected mean of a pair of reciprocal backcrosses is the same as that of F_2 generation of the cross between the two parents provided the differential loci are independent in their action (Jinks, 1956). Therefore, assuming no non-allelic interaction, the expected statistics for the analysis of backcross family means in a diallel set are the same as those for F_2 family means.

In Appendix II there are eighty backcrosses including reciprocals. A complete diallel table for these backcrosses therefore requires an amalgamation of four backcrosses to compute the appropriate means for each of the off-diagonal cells in the diallel matrix. Using the same symbols as in Appendix II, and taking any two parents, the appropriate backcross combinations can be shown to be equivalent to the mean of the corresponding F_2 hybrid. Thus the mean of $M(M \times CH)$, $(M \times CH)M$, $CH(M \times CH)$ and $(M \times CH)CH$ means is equivalent to the $(M \times CH)F_2$ mean, while the mean of $M(CH \times M)$, $(CH \times M)M$, $CH(CH \times M)$ and $(CH \times M)CH$ means is equivalent to the mean of its reciprocal, i.e., $(CH \times M)F_2$ hybrid.

Denoting the parents Marquis, Chinook, Khush-hal, Ciano and Inia as 1, 2, 3, 4 and 5 the following two diallel tables (Tables 40, 41) may be constructed, the one by keeping the parents of rows as recurrent parents and the other by keeping the parents of columns as recurrent parents. The numbers in the brackets in Table 40 and Table 41 denote the F_1 hybrids while those outside the brackets denote the recurrent parents. From these two tables a complete diallel table can be constructed which will correspond statistically to the F_2 diallel table

TABLE 40

Arrangement of backcrosses and reciprocals
in which the parents of rows are kept as recurrent parents.

	1	2	3	4	5
1.	11	11(12) + (12)11	11(13) + (13)11	11(14) + (14)11	11(15) + (15)11
2.	22(21) + (21)22	22	22(23) + (23)22	22(24) + (24)22	22(25) + (25)22
3.	33(31) + (31)33	33(32) + (32)33	33	33(34) + (34)33	33(35) + (35)33
4.	44(41) + (41)44	44(42) + (42)44	44(43) + (43)44	44	44(45) + (45)44
5.	55(51) + (51)55	55(52) + (52)55	55(53) + (53)55	55(54) + (54)55	55

TABLE 41

Arrangement of backcrosses and reciprocals
in which the parents of columns are kept as the recurrent parents.

	1	2	3	4	5
1.	11	22(12) + (12)22	33(13) + (13)33	44(14) + (14)44	55(15) + (15)55
2.	11(21) + (21)11	22	33(23) + (23)33	44(24) + (24)44	55(25) + (25)55
3.	11(31) + (31)11	22(32) + (32)22	33	44(34) + (34)44	55(35) + (35)55
4.	11(41) + (41)11	22(42) + (42)22	33(43) + (43)33	44	55(45) + (45)55
5.	11(51) + (51)11	22(52) + (52)22	33(53) + (53)33	44(54) + (54)44	55

and may therefore be used for the analysis of genetic components of variation as described by Jinks (1956). Thus, for example, if the entry $[11(12) + (12)11]$ above the main diagonal in Table 40 is denoted as x and the corresponding entry $[22(12) + (12)22]$ in Table 41 as y , then the corresponding element of the F_2 diallel table would be $1/2[1/2x + 1/2y] = 1/4(x + y)$. The entries in the remaining cells of the F_2 diallel table are obtained in the same way. Such a table may be called a *synthetic F_2 diallel table*.

Simple coefficients of correlation between the characters on the basis of the *synthetic complete F_2 diallel table* are given in Table 42. Onset-of-heading was positively correlated with final heading plant height, number of tillers per plant, number of spikelets per spike at both locations. It was negatively correlated with weight of seeds per spike at Parkland and 1000-kernel weight at both locations. The correlations with heading-span and yield per plant at both locations and with weight of seeds per spike at Ellerslie were not significant. The correlations of final heading and heading-span with other characters may be interpreted in the same way.

Plant height was positively correlated with number of tillers per plant, number of spikelets per spike at both locations and with number of seeds per spike at Ellerslie. It was negatively correlated with weight of seeds per spike and 1000-kernel weight at both locations. No correlations were observed between plant height and yield per plant at either location or with number of seeds per spike at Parkland.

Number of tillers per plant was positively associated with

TABLE 42

Simple correlation coefficients between ten characters
from backcross diallel set at two locations.

Character	2	3	4	5	6	7	8	9	10
1. Onset-of-heading	0.917** 0.830**	0.214 -0.025	0.727** 0.714**	0.332** 0.565**	0.592** 0.498**	0.327** 0.291**	-0.209 -0.289*	-0.607** -0.627**	-0.118 -0.011
2. Final heading	-	0.576** 0.532**	0.818** 0.720**	0.395** 0.671**	0.598** 0.550**	0.292** 0.254*	-0.305** -0.332**	-0.679** -0.631**	-0.179 0.096
3. Heading-span		-	0.507** 0.211	0.270** 0.341**	0.218 0.238*	-0.009 0.027	-0.362* -0.162	-0.431** -0.199	-0.233* 0.325**
4. Plant height			-	0.458** 0.538**	0.710** 0.650**	0.262* 0.169	-0.303** -0.470**	-0.638** -0.708**	0.006 -0.106
5. Number of tillers per plant				-	0.305** 0.411**	-0.041 0.216	-0.132 -0.289*	-0.094 -0.531**	0.491** 0.173
6. Number of spikelets per spike					-	0.604** 0.651**	0.115 0.105	-0.405** -0.460**	0.149 0.212
7. Number of seeds per spike						-	0.621** 0.600**	-0.160 -0.212	0.116 0.236*
8. Weight of seeds per spike							-	0.638** 0.644**	0.365** 0.444**
9. 1000-kernel weight								-	0.400** 0.333**
10. Yield per plant									-

First reading under each column refers to Ellerslie and second to Parkland.

* Significant at 5% level

**Significant at 1% level

number of spikelets per spike at both locations and with yield per plant at Ellerslie. It was negatively correlated with weight of seeds per spike and 1000-kernel weight at Parkland. There was no correlation with number of seeds per spike at either location or with weight of seeds per spike and 1000-kernel weight at Ellerslie and yield per plant at Parkland. The correlations of number of spikelets per spike, number of seeds per spike, weight of seeds per spike and 1000-kernel weight respectively with other characters may be interpreted in the same way.

Yield per plant was positively correlated with 1000-kernel weight and weight of seeds per spike at both locations, with number of seeds per spike and heading-span at Parkland and with number of tillers per plant at Ellerslie. It was negatively correlated with heading-span at Ellerslie. Correlations with onset-of-heading, final heading and plant height at both locations were not significant.

The results of the factor analysis as the factor loadings of the varimax-rotated five factor matrix are given in Table 43. Approximately 93% of the total variability at both locations was explained by these factors.

The first principal factor was termed *lateness* because of its highest loadings for onset-of-heading and final heading at both locations. This factor negatively contributed towards weight of seeds per spike, 1000-kernel weight and yield per plant at both locations thus confirming the inverse relationship between time of maturity and yield as observed for F_1 and F_2 diallel data. Plant height at Ellerslie and number of tillers per plant contributed proportionately more towards

TABLE 43

Varimax rotated factor matrix for ten characters
from backcross diallel set at two locations.

Character	Communality	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5
Onset-of-heading	0.986 0.913	0.958 0.721	0.154 0.561	0.023 0.061	0.210 -0.118	-0.005 -0.248
Final heading	0.982 0.885	0.869 0.709	0.135 0.532	0.026 0.024	0.252 -0.009	0.380 0.314
Heading-span	0.987 0.965	0.182 0.171	-0.040 0.109	-0.016 -0.038	0.180 0.139	0.959 0.951
Plant height	0.868 0.915	0.621 0.397	0.216 0.847	0.252 -0.086	0.501 -0.163	0.348 0.074
Number of tillers per plant	0.883 0.859	0.380 0.883	-0.139 0.152	0.812 0.054	0.009 0.027	0.243 0.227
Number of spikelets per spike	0.868 0.914	0.415 0.173	0.659 0.768	0.261 0.511	0.426 0.068	0.105 0.169
Number of seeds per spike	0.924 0.981	0.205 0.168	0.937 0.211	-0.048 0.952	-0.024 0.029	-0.004 0.012
Weight of seeds per spike	0.984 0.959	-0.188 -0.274	0.702 -0.266	0.103 0.732	-0.642 0.498	-0.184 -0.169
1000-kernel weight	0.911 0.892	-0.473 -0.489	-0.003 -0.502	0.232 -0.012	-0.768 0.601	-0.208 -0.199
Yield per plant	0.898 0.904	-0.182 0.092	0.193 0.021	0.880 0.167	-0.123 0.899	-0.196 0.244
Percent of total	92.910	29.523	19.529	16.343	15.894	13.714
Variability explained	91.870	23.700	23.085	19.029	14.832	12.771

First reading under each column refers to Ellerslie and second to Parkland.

lateness than either the number of spikelets per spike or number of seeds per spike at both locations. *Lateness* explained 29% and 23% of the total variation present in the data for Ellerslie and Parkland respectively.

Number of spikelets per spike, number of seeds per spike and weight of seeds per spike could be grouped into the second factor *yielding ability* at Ellerslie, because of their higher contribution to this factor. At Parkland, this factor was termed *height* since it carried maximum loading for that character. Both the factors explained 19% and 23% variability in the data at respective locations. At Ellerslie, other yield components such as number of tillers per plant and 1000-kernel weight negatively contributed towards *yielding ability* confirming the results of Table 42. At Parkland, onset-of-heading, final heading and number of spikelets per spike had proportionately higher contributions towards *height* while weight of seeds per spike and 1000-kernel weight turned out to be the negative contributors to this factor.

Yield at Ellerslie and *seeds per spike* at Parkland were classified as the third principal factor which explained 16% and 19% of the total variability for respective locations. At Ellerslie, only number of tillers per plant contributed appreciably towards *yield*, otherwise the contributions of number of spikelets per spike, number of seeds per spike, weight of seeds per spike and 1000-kernel weight were comparatively low. The factor *lateness* also made a very poor contribution towards *yield*. At Parkland, number of spikelets per spike

and weight of seeds per spike were the major contributors towards *seeds per spike*. Plant height and 1000-kernel weight were negatively affected by this factor.

The term *low yield* was selected for the fourth factor at Ellerslie because of the negative loadings for number of seeds per spike, weight of seeds per spike, 1000-kernel weight, yield per plant and the fact that the lowest positive value was found for number of tillers per plant. At Parkland the alternative fourth principal factor was chosen as *high yield* as it carried the highest loading for yield per plant and positive loadings for 1000-kernel weight, weight of seeds per spike, number of seeds per spike, number of spikelets per spike and number of tillers per plant. Onset-of-heading and final heading contributed positively toward *low yield* but negatively toward *high yield*. Plant height revealed an inverse relationship with respect to its contribution towards the yield factor at both locations.

The fifth principal factor, classified as *heading period*, explained 13% of the total variation at both locations. It carried maximum loadings for heading-span at both locations. The contribution of yield and its components, viz., number of spikelets per spike, number of seeds per spike, weight of seeds per spike and 1000-kernel weight towards *heading period* was either very low or negative at both locations, indicating an inverse relationship of yield with heading period. The negative contribution of initial heading towards this factor indicates that earlier heading entries take a longer period to complete

TABLE 44

Estimates of general combining ability of five parental lines
used in backcross diallelset for ten characters at two locations.

Character	Marquis	Chinook	Khush-hal	Ciano	Inia
Onset-of-heading	1.8350 1.9650	1.1600 1.4316	-0.1316 -0.0350	-1.5753 -2.4850	-1.2899 -0.8766
Final heading	2.3333 1.8967	1.4667 2.1800	-0.0166 -0.3450	-1.8500 -2.2034	-1.9333 -1.5283
Heading-span	0.4667 -0.0417	0.4167 0.7750	0.0917 -0.3500	-0.3083 0.2417	-0.6667 -0.6250
Plant height	14.2345 14.8495	9.9832 10.2860	-7.6700 -8.0976	-6.3678 -7.7471	-10.1798 -9.2909
Number of tillers per plant	0.3025 1.0841	0.6791 0.4932	0.2759 0.0704	-0.2361 -0.5536	-1.0213 -1.0940
Number of spikelets per spike	0.8035 0.6312	0.2629 0.2373	-0.4382 -0.3260	-0.5110 -0.5021	-0.1172 -0.0404
Number of seeds per spike	3.5835 2.0422	-1.8660 -1.2955	-1.1196 0.5107	-2.1986 -2.4295	1.6006 1.1722
Weight of seeds per spike	-0.0059 -0.0342	-0.1185 -0.0813	-0.0222 0.0577	-0.0306 -0.0309	0.1771 0.0888
1000-kernel weight	-2.6314 -2.3445	-1.2960 -0.7879	0.3155 0.9186	1.4580 1.4448	2.1540 0.7690
Yield per plant	0.0570 -0.4831	-0.7077 0.2377	-0.6801 -0.0136	0.3461 -0.0030	0.9848 0.2419

First reading under each column refers to Ellerslie and second to Parkland.

their maturity. This kind of relationship was found to be in contradiction with the results obtained for F_1 and F_2 diallels.

Combining ability analysis

The general combining ability values of the parental lines used in the backcross diallel are given in Table 44. At both locations, Marquis ranked first in GCA for onset-of-heading and Ciano the lowest, and therefore these parents were regarded as being late and early maturing respectively. Similar interpretations may be given for final heading and heading-span. For plant height, Marquis and Inia at both locations ranked highest and lowest respectively, while for tiller number Chinook at Ellerslie and Marquis at Parkland scored highest. At both locations, Marquis and Ciano possessed the highest and the lowest GCA for number of spikelets per spike and number of seeds per spike respectively. Similar interpretations may be given for other yield components. As far as yield is concerned, at both locations Inia may be regarded as the best combiner, while Chinook at Ellerslie and Marquis at Parkland were the poorest.

The values of specific combining ability for heading data are given in Tables 45, 46 and 47. The results of Table 45 show that the cross (CxI) possessed the highest SCA and (MxI) the lowest at both locations. The best hybrid was associated with the parents with the lowest GCA's at both locations and the worst was from parents with the highest GCA's. The variances for GCA's were larger than those for SCA's. The reciprocal effects were not significant in all cases. Similar

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from backcross diallel set at two locations.

TABLE 45. Onset-of-heading

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano			
Marquis	-	0.5067 -0.1399	-0.7017 0.0351	-0.9267 -0.5150	1.8350 1.9650	3.3042 3.7204	-0.1577 -0.3519
Chinook	-0.2917 -0.5833	-	-0.5267 0.1100	-0.9600 -1.1483	1.1600 1.4316	1.2825 1.9089	-0.0721 -0.3453
Khush-hal	0.0417 -0.1250	-0.4583 -0.6667	-	0.3733 -0.2233	-0.1316 -0.0350	-0.0458 -0.1395	0.0989 -0.3474
Ciano	-0.2917 -0.7083	0.3333 -0.2083	0.0417 0.0	-	-1.5733 -2.4850	2.4122 6.0344	0.4822 0.1927
Inia	-0.1667 0.0417	-0.0833 0.0	0.0 0.1667	0.0 -0.0417	-1.2899 -0.8766	1.6009 0.6277	1.2834 0.5468

Reciprocal effects

TABLE 46. Final heading

Marquis	-	0.8584 -0.3133	-0.5333 -0.7883	-0.2417 -0.8883	-1.7000 -0.8967	2.3333 1.8967	5.3936 3.4204	-0.1267 -0.4424
Chinook	-0.2093 -1.0000	-	-0.5416 -0.2383	-0.5000 -1.1716	-0.5000 -0.9330	1.4667 2.1800	2.1004 4.5753	0.1189 -0.4097
Khush-hal	0.2500 0.1667	-0.6250 -0.1667	-	-0.4333 0.6451	0.1917 0.3450	-0.0166 -0.3450	-0.0504 -0.0579	0.0658 0.2758
Ciano	-0.2083 -0.1250	0.0833 -0.3750	0.1667 0.6667	-	0.8584 0.4117	-1.8500 -2.2034	3.3718 4.6779	0.0387 0.4169
Inia	0.3333 0.2083	0.1667 0.3750	0.0417 0.2083	0.1250 -0.1667	-	-1.9333 -1.5283	3.6871 2.1588	1.1777 0.2101

Reciprocal effects

First reading under each column refers to Ellerslie and the second to Parkland.

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from backcross diallel set at two locations.

TABLE 47. Heading-span

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia		
Marquis	-	0.2500 -0.2000	0.2000 -0.7833	0.6833 -0.3333	-0.2500 0.4500	0.4667 0.0417	-0.1442 -0.5003
Chinook	0.0833 -0.4167	-	-0.1250 -1.3083	0.3583 0.0167	0.3000 -0.0750	0.4167 0.7750	-0.1234 -0.4870
Khush-hal	0.2083 0.2917	-0.1667 0.5000	-	-0.7750 0.6417	-0.1667 0.3000	0.0917 -0.3500	-0.1257 0.2748
Ciano	0.0417 0.5833	-0.2500 -0.1667	0.1250 0.3333	-	-0.2676 0.2917	-0.3083 0.2417	0.2544 -0.3259
Inia	0.5000 0.1667	0.2500 0.3750	0.0417 0.0417	0.1250 -0.1250	-	-0.6667 -0.6250	-0.0604 -0.3726

Reciprocal effects

TABLE 48. Plant height

Marquis	-	1.2204 -1.5368	2.4292 6.4507	0.7733 3.8329	-5.9562 -4.4574	14.2345 14.8495	201.2519 218.5630	-3.4246 -4.8617
Chinook	1.6708 -0.9280	-	0.2537 -0.4441	0.8719 0.9886	1.8012 -1.2487	9.9832 10.2860	98.2939 103.8567	-2.9272 -4.0744
Khush-hal	2.0138 1.1430	-1.9303 -2.0403	-	-2.2625 -1.2273	1.5805 -0.0541	-7.6700 -8.0976	57.4592 63.6259	-1.4352 9.0746
Ciano	-2.3949 -1.6303	-2.6567 -1.9159	0.6065 0.3160	-	0.5592 -0.9246	-6.3678 -7.7471	39.1798 58.0724	-1.2646 0.8631
Inia	4.3464* 4.2671*	2.5614 1.7700	0.8408 -0.0917	1.1077 0.1983	-	-10.1798 -9.2909	102.2588 84.3766	10.4201 2.5667

First reading under each column refers to Ellerslie and the second to Parkland.

*Significant at 5% level

Reciprocal effects

interpretations for Tables 46 and 47 may be made.

Hybrids (MxK) and (MxI) showed the highest and the lowest SCA for plant height (Table 48) at both locations. The best hybrid at both locations was associated with the parent (Khush-hal) with the second lowest GCA, and the poorest hybrid was associated with one parent (Marquis) having the highest GCA and another (Inia) showing the lowest GCA at both locations. The variances for GCA were greater than those for SCA and the reciprocal effects at both locations were significant only for (IxM). This effect was attributed to the female parent because of the positive sign appended to it.

At both locations, hybrid (CxI) had the highest SCA while (KxI) at Ellerslie and (MxI) at Parkland ranked lowest and produced the lowest number of tillers per plant (Table 49). The best hybrid had a parent with the lowest GCA at both locations, while the poorest ranking hybrids had high GCA parents (Marquis and Khush-hal, respectively). The reciprocal effects were non-significant for all hybrids and GCA variances were usually higher than those for SCA, except for Marquis, Khush-hal and Ciano, all at Ellerslie. The larger SCA variances for the latter parents imply an importance of non-additive gene effects for number of tillers per plant, and reveal instability in the performance of their hybrids.

The results for the other components of yield, such as number of spikelets per spike (Table 50), number of seeds per spike (Table 51) weight of seeds per spike (Table 52) and 1000-kernel weight (Table 53) may be interpreted in a similar way.

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from backcross diallel set at two locations.

TABLE 49. Number of tillers per plant

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia		
Marquis	-	0.0587 -0.2333	0.1659 -0.6416	-0.2478 -0.3376	-0.0077 -0.7573	0.3025 1.0841	-0.4126 -0.4296
Chinook	-0.5267 -0.2190	-	0.2268 -0.3882	0.4683 -0.2684	-0.2315 0.0716	0.6791 0.4932	-0.4114 -0.4114
Khush-hal	0.4750 0.3750	0.0875 0.2375	-	-0.2497 0.2336	-0.6937 -0.2010	0.2759 0.0704	-0.3863 -0.2422
Ciano	-0.1367 -0.2033	-0.5357 0.2167	0.1792 -0.1958	-	0.4877 0.3607	-0.2361 -0.5536	-0.2982 -0.3494
Inia	0.2042 0.2448	-0.0013 0.0412	-0.2167 -0.0958	0.6943 0.1668	-	-1.0213 -1.0940	-0.1550 -0.1799

Reciprocal effects

TABLE 50. Number of spikelets per spike

Marquis	-	0.3819 0.1083	0.2495 0.4159	-0.0846 0.0875	-0.3061 -0.0067	0.8035 0.6312	-0.0831 -0.0845
Chinook	-0.0993 0.0138	-	0.1926 -0.3419	-0.0259 0.2164	-0.1115 0.1788	0.2629 0.2373	-0.0345 -0.0805
Khush-hal	0.4042 0.1975	-0.1623 -0.1708	-	0.1214 0.0086	-0.0359 0.0971	-0.4382 -0.3260	-0.0500 0.0122
Ciano	-0.2898 0.1233	-0.1850 0.2027	0.0875 0.1573	-	0.0676 -0.1626	-0.5110 -0.5021	-0.0756 -0.0663
Inia	0.0335 0.3435	0.0988 0.3020	0.1557 0.0598	0.1650 -0.0790	-	-0.1172 -0.0404	-0.0457 -0.0618

Reciprocal effects

First reading under each column refers to Eilerslie and the second to Parkland.

Estimates of specific combining ability, reciprocal effects and variances
of general and specific combining ability from backcross diallel set at two locations.

TABLE 51. Number of seeds per spike

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano			
Marquis	-	0.1015 0.2519	0.0655 0.1132	0.4011 0.8717	-1.3428 0.3590	3.5835 2.0422	-1.9664 -1.0532
Chinook	0.1910 -0.6400	-	-0.3113 -1.5280	0.0544 0.2122	0.0701 1.3177	-1.8660 -1.2955	-1.9630 -1.0321
Khush-hal	0.8403 0.7335	-0.7640 0.4013	-	-0.9921 -0.8981	0.2122 0.0125	-1.1196 0.5107	-1.9327 -0.2707
Ciano	-1.1300 0.7405	-1.0005 0.4957	-0.5227 1.0112	-	1.8083 -0.2557	-2.1986 -2.4295	-1.5837 -0.5161
Inia	-0.4867 0.3572	0.0820 0.0558	-0.2068 0.3265	-1.2177 -0.5962	-	1.6006 1.1722	-0.2588 -0.4097

Reciprocal effects

TABLE 52. Weight of seeds per spike

Marquis	-	0.0490 0.0461	-0.0080 -0.0314	-0.0624 0.0606	-0.0289 0.0699	-0.0059 -0.0342	-0.0074 -0.0039
Chinook	0.0552 0.0048	-	-0.0406 -0.0746	-0.0150 0.0018	-0.0264 0.0180	-0.1185 -0.0813	-0.0066 -0.0032
Khush-hal	0.0022 0.0150	-0.0190 0.0120	-	0.0007 -0.0103	0.0178 -0.0050	-0.0222 0.0577	-0.0068 -0.0017
Ciano	-0.0810 0.0340	-0.0268 0.0335	-0.0028 0.0553	-	0.0589 -0.0137	-0.0306 -0.0309	-0.0068 -0.0027
Inia	-0.0638 -0.0573	0.0252 -0.0090	-0.0277 0.0240	-0.0853 -0.0190	-	0.1771 0.0888	-0.0056 -0.0021

Reciprocal effects

First reading under each column refers to Ellerslie and the second to Parkland.

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from backcross diallel set set at two locations.

TABLE 53. 1000-kernel weight

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia		
Marquis	-	0.6721 0.8088	-0.3252 -0.7960	-0.8322 0.4879	0.3192 1.4128	6.4507 5.0647	-1.1837 -1.0796
Chinook	0.9477 0.4982	-	-0.5640 -0.5859	-0.4496 -0.1117	-0.4911 -0.5019	1.2062 0.1889	-1.0332 -0.8615
Khush-hal	-0.5490 -0.1602	0.3412 0.0255	-	0.5533 0.8728	0.3476 -0.0248	-0.3740 0.4120	-1.0425 -0.7540
Ciano	0.5182 0.4008	0.1213 0.3108	0.5002 -0.0305	-	-0.5193 -0.1230	1.6523 1.6556	-0.7835 -0.7422
Inia	-0.8622 -1.3710	0.5862 -0.2628	-0.1982 0.2245	-0.7360 -0.0462	-	4.1662 0.1496	-0.9392 -0.3250

Reciprocal effects

TABLE 54. Yield per plant

Marquis	-	0.5268 0.6335	0.1073 -0.0471	-0.2387 -0.3599	-0.6415 0.0177	-0.3228 0.0377	-0.8150 -0.4891
Chinook	0.7010 -0.4425	-	0.6673 -0.6144	-0.0782 -0.2531	-0.6920 0.0680	0.1748 -0.1292	-0.7225 -0.3553
Khush-hal	0.3322 0.1092	-0.1002 0.6103	-	0.2599 0.5103	-1.2433 -0.7849	0.1365 -0.1995	-0.6627 -0.3625
Ciano	-0.3313 0.5293	-0.8415 0.0917	0.7498 0.6003	-	0.3511 0.0547	-0.2062 -0.1956	-0.7715 -0.3378
Inia	-0.6825 -0.8422	0.2547 0.7200	-0.4963 0.0107	1.1603 0.1920	-	0.6438 -0.1371	0.0374 -0.2811

Reciprocal effects

First reading under each column refers to Ellerslie and the second to Parkland.

TABLE 55

Analysis of variance of general and specific combining ability and reciprocal effects
for ten characters from backcross diallel set at two locations.

Character	M.S. for GCA	M.S. for SCA	M.S. for reciprocal effects	Error M.S.
Onset-of-heading	22.1406** 32.1406**	2.5500** 2.3875**	0.1059 0.2753	0.2363 0.5273
Final heading	36.8594** 39.1250**	1.7687** 3.8375**	0.1462 0.3823	0.1901 0.6637
Heading-span	2.3482** 2.9344**	0.5423* 1.2388	0.0976 0.2347	0.2164 0.7498
Plant height	1263.1875** 1345.4687**	13.8687** 26.5062**	10.2239 6.8296	5.1350 7.2887
Number of tillers per plant	4.3223** 7.3193**	0.3368 0.9020	0.2838 0.0941	0.6138 0.6445
Number of spikelets per spike	2.9551** 2.0391**	0.1430 0.1289	0.0776 0.0736	0.1247 0.1266
Number of seeds per spike	62.4219** 33.4844**	1.6523 2.1719	1.1293 0.7036	2.9885 1.5811
Weight of seeds per spike	0.1172** 0.0499**	0.0032 0.0078	0.0047 0.0020	0.0110 0.0058
1000-kernel weight	38.6875** 24.1055**	0.8004 1.5766	0.7034 0.5068	1.7762 1.6191
Yield per plant	5.1455** 0.9004	1.2141 0.5074	0.7258 0.5015	1.2218 0.7331

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level

**Significant at 1% level

In yield per plant (Table 54), cross (MxCH) had the highest SCA and consequently was the highest yielding at both locations, while cross (KxI) was the lowest yielding as it had the lowest SCA. The highest yielding hybrid had the parents (Marquis at Parkland and Chinook at Ellerslie) with the lowest GCA, while the poor yielding cross (KxI) had one parent (Khush-hal) with the lowest and one (Inia) with the highest GCA at both locations. The GCA variances were higher than those for SCA only for Marquis at Parkland and Chinook, Khush-hal and Inia at Ellerslie. The reciprocal effects were non-significant in all cases.

The analysis of variance for general and specific combining ability together with the reciprocal effects (Table 55) reveals important additive gene effects for all the characters at both locations, with the exception of yield per plant at Parkland. Thus the significance of mean squares for GCA's substantiates the differences among the parental lines. The significant mean squares for SCA's for onset-of-heading, final heading and plant height at both locations and heading-span at Ellerslie suggest a relatively greater importance of SCA over GCA. Thus for earliness and plant height, selection for SCA should be given priority in breeding programmes aimed at evolving desired lines.

Diallel cross analysis

Preceding the analysis, the validity of the assumption of no reciprocal differences was tested by means of Hayman's (1954a) analysis of variance. The results are given in Table 56. Heading-span at Ellerslie and plant height at Parkland showed a significant

TABLE 56

Mean squares from the analysis of variance
of 5 x 5 backcross diallel set for ten characters at two locations.

Source of variation	D.F.	Onset-of-heading	Final heading	Heading-span	Plant height	Number of tillers per plant	Number of spikelets per spike	Number of seeds per spike	Weight of seeds per spike	1000 kernel weight	Yield per plant
a	4	66.5313** 96.3906**	110.6094** 117.4531**	7.0449** 8.8047*	3790.0000** 4037.0000**	12.9570* 21.9541**	8.6552** 6.1113*	187.3125** 100.3906**	0.2514* 0.1495*	115.9844** 72.2969**	15.4229** 2.6934
b	10	7.6625** 7.1937**	5.3062 11.5375**	1.6266 3.7156	41.5000* 79.3000*	1.0152 2.7094	0.4316 0.2918	5.0000 6.5812	0.0098 0.0234	2.4312 4.7312	3.6477 1.5289
b_1	1	27.4519 45.4352	19.3802* 69.8419	0.1302 3.0000	4.8411 5.6988	0.0016 14.0152	0.5952 1.0854	0.0135 0.6248	0.0091 0.0113	4.9872 6.2116	2.8834 1.8030
b_2	4	4.5937* 3.8926	1.3437 7.8437	2.8215 6.3035	33.0156 120.1719	1.2312 2.6053	0.6533 0.2109	4.7842 12.2314	0.0036 0.0489	1.3271 5.3594	5.6904 1.1279
b_3	5	6.1500** 2.1875	5.6250** 2.8375	0.9711 1.7891*	55.6125 61.6000**	1.0469 0.5344	0.2281 0.4039*	6.2000 3.2625	0.0149 0.0055	2.8000 3.9750**	2.1734 1.7984
c	4	0.2365 1.1062	0.2542 0.7573	0.4969* 0.8417	46.9664 18.1423*	0.6718 0.4849	0.1605 0.3921	2.9725 3.6308	0.0112 0.0083	1.5768 1.0007	1.0532 1.4769
d	6	0.3719 0.6392	0.5615 1.4066	0.1566 0.6125	19.8087 22.0532	0.9712 0.1470	0.2808 0.1070	3.6648 1.0973	0.0160 0.0045	2.4660 1.8668	2.9268 1.5227
Blocks x a	8	1.1953 1.5703	0.6484 2.2578	0.8897 2.5236	14.9219 38.5859	2.4395 2.3799	0.9517 0.8940	17.9219 8.5703	0.0558 0.0238	11.2734 4.4165	1.6191 3.7525
Blocks x b	20	0.9625 1.9500	0.8375 3.5156	0.8468 3.5586	19.8469 28.0469	2.4242 2.5652	0.2797 0.4021	8.5250 5.5062	0.0360 0.0257	6.3781 7.2645	5.4461 2.5219
Blocks x b_1	2	0.3787 9.2654	0.9554 25.2762	1.5654 5.1350	13.4377 217.9866	3.3930 25.4726	0.8469 0.0840	31.8310 0.5820	0.0879 0.0585	4.1877 17.8517	16.2239 0.1980
Blocks x b_2	8	0.9814 1.8823	0.8145 3.8979	1.0515 7.5884	26.3594 33.3281	4.8573 2.5774	0.2700 0.8656	9.7495 11.6685	0.0580 0.0530	13.1274 15.1216	7.6665 4.5089
Blocks x b_3	10	0.5062 1.4375	0.9625 1.8312	0.6952 0.5326	17.3562 7.5562	0.6228 0.5187	0.2527 0.9073	6.0687 1.2094	0.0167 0.0032	1.8535 0.6453	3.1770 1.4113
Blocks x c	8	0.2818 1.3125	0.2979 0.3089	0.1000 0.9120	13.7982 4.0308	0.9417 1.9616	0.1508 0.2277	5.0430 3.6050	0.0118 0.0098	1.5511 5.2596	3.5782 1.8341
Blocks x d	12	0.2427 1.1632	0.2771 0.3983	0.5253 0.7844	9.5492 12.6719	1.1389 0.5639	0.2996 0.1085	5.9280 2.0342	0.0276 0.0053	2.1627 0.9139	2.1360 0.8813
Error	48	0.7079 1.5838	0.5759 1.9922	0.6491 2.2514	15.4430 21.9569	1.8584 1.9246	0.3752 0.3817	8.8616 4.7487	0.0332 0.0176	5.3357 4.8681	3.6694 2.2023

* Significant at 5% level

**Significant at 1% level

First reading under each column refers to Ellerslie and second to Parkland. Error D.F. comprises of block interaction with D.F. of (a+b+c+d). Each component has been tested against its own block interaction.

TABLE 57

Analysis of variance of $N_p - V_p$ for ten characters
from backcross diallel set at two locations.

Character	Block M.S.	Entry M.S.	Error M.S.
Onset-of-heading	4.9320 16.4215	1.5831* 1.6003*	0.3734 0.8179
Final heading	0.2722 38.3562	0.7335* 2.5496	0.1721 1.9131
Heading-span	0.5333 1.1121	0.0653 0.7220	0.2203 1.1063
Plant height	12060.9687 9119.5000	309.5469 303.1406*	229.9219 77.2656
Number of tillers per plant	6.5381 1.0551	0.4283 0.6511	0.7682 0.8967
Number of spikelets per spike	0.3822 0.0070	0.0215 0.0133	0.0078 0.0426
Number of seeds per spike	426.5688 54.6648	9.7215 3.2239	13.6523 4.9508
Weight of seeds per spike	0.0049 0.0021	0.0002 0.00	0.0002 0.00
1000-kernel weight	205.2457 38.0292	2.3595 1.3192	3.4383 4.8242
Yield per plant	6.7847 0.2112	1.9057 0.7162	2.6477 0.9051

First reading under each column refers to Ellerslie and second to Parkland.

*Significant at 5% level

TABLE 58

Estimates of second degree statistics
for ten characters from backcross diallel set at two locations.

Character	V_{OLO}	W_{OLO2}	V_{OL2}	V_{LL2}	$(W_{L1} - W_{LO})^2$
Onset-of-heading	15.0000 15.7002	5.7395 6.6334	2.2227 3.2148	3.4973 4.4137	1.4641 2.4233
Final heading	16.9668 27.1514	7.8656 10.1422	3.6934 3.9199	4.5766 5.8430	1.0336 3.7249
Heading-span	0.5889 3.6111	0.2610 0.8947	0.2349 0.2936	0.5060 0.9129	0.0069 0.1600
Plant height	486.7740 518.4434	246.3824 258.1760	126.3408 134.5703	133.2646 147.5088	0.2528 0.3040
Number of tillers per plant	1.4343 5.4749	0.7289 1.9703	0.4319 0.7317	0.6010 1.1834	0.0003 0.7475
Number of spikelets per spike	1.2283 0.5749	0.5699 0.3369	0.2957 0.2039	0.3676 0.2692	0.0317 0.0578
Number of seeds per spike	28.9980 12.2275	13.2521 5.7904	6.2422 3.3457	7.0721 4.4383	0.0007 0.0333
Weight of seeds per spike	0.0384 0.0360	0.0211 0.0116	0.0117 0.0050	0.0133 0.0089	0.0004 0.0006
1000-kernel weight	16.7744 13.1670	7.9937 5.4328	3.8662 2.4092	4.2670 3.1975	0.2660 0.3312
Yield per plant	5.4553 0.8875	1.5937 0.2552	0.5142 0.0899	1.1225 0.3447	0.1538 0.0961

First reading under each column refers to Ellerslie and second to Parkland.

c component, indicating significant reciprocal differences. Significance for a confirms the existence of parental differences for all characters at both locations, with the exception of yield per plant at Parkland. Significance of b shows that dominance is present for onset-of-heading, final heading and plant height at both locations while b_1 shows that dominance is directional for final heading at Ellerslie. Other assumptions underlying the diallel analysis were tested by analysis of variance of $W_r - V_r$ differences. The heterogeneity of $W_r - V_r$ over arrays for onset-of-heading and heading-span at Ellerslie and plant height at Parkland (Table 57) indicates non-validity of at least one of the assumptions; no multiple allelism, uncorrelated gene distribution and no non-allelic gene interaction. This situation is discussed later, during the graphical analysis of these characters.

The estimates of second degree statistics calculated from array variances and parent-offspring covariances are presented in Table 58. The genetic components of variation were computed according to Johnson and Aksel's (1959) procedure, where the effects of heterozygote is halved because the backcross entries were made equal to those of F_2 's (Jinks, 1956). The estimates of genetic components of variation are given in Table 59. Significance was tested in a manner similar to that used for F_2 's. Proportional estimates of genetic parameters, calculated from Table 59 are presented in Table 60. The interpretation of the results in Tables 59 and 60, together with, the graphical analysis of the data for all the characters under study is as follows:

Except E at Ellerslie and F at Parkland, all components

TABLE 59
Estimates of genetic components of variation
from backcross diallel set for ten characters at two locations.

Character	D	F	H_1	H_2	h	E
Onset-of-heading	14.7635 ± 0.5161** 13.9224 ± 0.5422**	6.7593 ± 1.2892** 1.7335 ± 1.3543	5.4162 ± 1.3938** 4.1991 ± 1.4642**	4.6253 ± 1.2642** 3.7397 ± 1.3280**	5.7051 ± 0.8535** 9.3553 ± 0.8966**	0.2364 ± 0.2107 0.5278 ± 0.2213*
Final heading	16.7767 ± 0.4881** 25.8080 ± 0.1919**	2.2430 ± 1.2193 11.5783 ± 0.4993**	3.3163 ± 1.3182** 7.5494 ± 0.5398**	3.1526 ± 1.1956** 6.3649 ± 0.4896**	4.0130 ± 0.8072** 14.4746 ± 0.3305**	0.1901 ± 0.1993 0.6636 ± 0.0816**
Heading-span	0.3726 ± 0.2020* 2.9149 ± 0.4003**	-0.0458 ± 0.5045 2.8513 ± 1.2247*	1.0865 ± 0.5455* 1.7867 ± 1.3240	0.6157 ± 0.4947 0.9762 ± 1.2009	-0.1107 ± 0.3340 0.1597 ± 0.8108	0.2164 ± 0.0825** 0.7505 ± 0.2001**
Plant height	481.6389 ± 6.3199** 511.1506 ± 11.9086**	-18.1432 ± 15.7872 -4.5684 ± 29.7476	20.9514 ± 17.0677 58.0338 ± 32.1602	17.4245 ± 15.4806 38.3688 ± 29.1700	-2.2538 ± 10.4517 -3.4512 ± 19.6940	5.1354 ± 2.5801** 7.2925 ± 4.8716
Number of tillers per plant	0.8154 ± 0.0969** 4.8305 ± 0.1501**	-0.7879 ± 0.2422** 2.2954 ± 0.3750**	-0.6063 ± 0.2618** 0.6520 ± 0.4054	-0.5614 ± 0.2375* 0.5180 ± 0.3677	-0.3957 ± 0.1603** 2.5775 ± 0.2482	0.6189 ± 0.0396** 0.6444 ± 0.0613**
Number of spikelets per spike	1.1037 ± 0.0589** 0.4482 ± 0.0313**	0.0273 ± 0.1472 -0.3498 ± 0.0782**	0.0948 ± 0.1591 -0.0253 ± 0.0845	0.0382 ± 0.1443 0.0080 ± 0.0767	0.0472 ± 0.0975 0.1504 ± 0.0518**	0.1246 ± 0.0241** 0.1267 ± 0.0128**
Number of seeds per spike	26.0484 ± 0.7304** 10.6477 ± 0.6544**	1.4479 ± 1.8244 -0.6025 ± 1.6346	-3.3914 ± 1.9724 2.7113 ± 1.7672	-2.5798 ± 1.7890 1.2106 ± 1.6028	-1.8849 ± 1.2078 -0.8779 ± 1.0822	2.9497 ± 0.2982** 1.5799 ± 0.2671**
Weight of seeds per spike	0.0273 ± 0.0007** 0.0302 ± 0.0017**	-0.0210 ± 0.0017** 0.0188 ± 0.0044**	-0.0215 ± 0.0019** 0.0101 ± 0.0047**	-0.0156 ± 0.0017** 0.0038 ± 0.0043	-0.0051 ± 0.0011** -0.0014 ± 0.0029	0.0111 ± 0.0003** 0.0059 ± 0.0007**
1000-kernel weight	14.9988 ± 0.1177** 11.5476 ± 0.3657**	-0.5569 ± 0.2940 2.6595 ± 0.9136**	-2.7492 ± 0.3178** 0.0153 ± 0.9877	-1.9481 ± 0.2882** -0.0856 ± 0.8958	-0.0724 ± 0.1946 0.2886 ± 0.6048	1.7756 ± 0.0480** 1.6194 ± 0.1493**
Yield per plant	4.2333 ± 0.3936** 0.1538 ± 0.1558	3.0700 ± 0.9832** -0.1264 ± 0.3892	0.3925 ± 1.0630 -0.6622 ± 0.4208	-0.0118 ± 0.9642 -0.4481 ± 0.3817	-0.1673 ± 0.6509 -0.6849 ± 0.2577	1.2225 ± 0.1607** 0.7336 ± 0.0631**

First reading under each column refers to Eilerslie and second to Parkland.

* Significant at 5% level

** Significant at 1% level

TABLE 60

Proportional estimates of genetic parameters
from the backcross diallel set for ten characters at two locations.

Character	$[H_1/D]^{1/2}$	$[H_2/4H_1]$	$\{(4DH_1)^{1/2} + F\} \div \{(4DH_1)^{1/2} - F\}$	h^2/H_2	$r_{y_r/w_r} + V_r$	Heritability
Onset-of-heading	0.6057* 0.5492*	0.2135* 0.2227*	2.2149* 1.2557*	1.2334 2.5016	0.9758 0.9398	1.0275 0.7527
Final heading	0.4446* 0.5409*	0.2377* 0.2108*	1.3539* 2.4173*	1.2729 2.2741	0.9486 0.9672	0.9003 1.0562
Heading-span	1.7077* 0.7829	0.1500 0.1366	0.9305† 4.3292	-0.1699 0.1636	0.6344 0.4387	0.1571 0.6007
Plant height	0.2086 0.3369	0.2079 0.1653	0.8343 0.9738	-0.1293 -0.0899	0.3243 -0.6073	0.8898 0.8477
Number of tillers per plant	0.9174 0.3674	0.2045 0.1986	0.3090 4.6612	0.7049 4.9754	0.8415 0.9151	0.2403 0.8379
Number of spikelets per spike	0.2931 0.2375	0.1007 -0.0787	1.0880 -0.2433	1.2373 18.8908	-0.5694 -0.8324	0.9423 0.3502
Number of seeds per spike	0.3608 0.5046	0.1902 0.1116	1.1669 0.8938	0.7306 -0.7552	-0.5376 0.2682	0.7891 0.5250
Weight of seeds per spike	0.8884 0.5775*	0.1814 0.0946	0.3949 3.3493*	0.3291 -0.3582	-0.1965 0.3449	0.3834 0.6696
1000-kernel weight	0.4281 0.0364	0.1772 -1.4023	0.9169 -1.9226	0.0371 -3.3718	0.5993 -0.4941	0.7533 0.7507
Yield per plant	0.3045 2.0749	-0.0075 0.1692	-11.4843 0.6694	14.1870 0.1894	0.9215 -0.4361	0.6567 0.0602

First reading under each column refers to Ellerslie and second to Parkland.

*Genetic components of variation for the characters are significantly different from zero ($P < 0.05$)

†Components D and H_1 significant, F non-significant ($P > 0.05$)

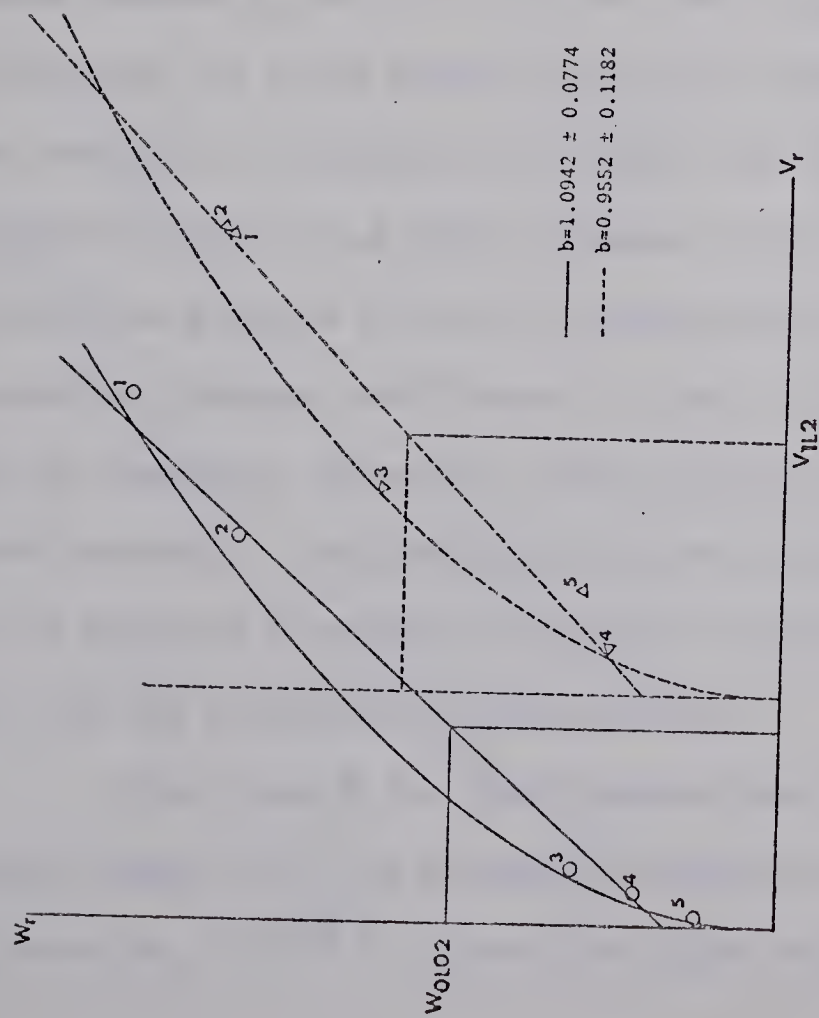


Figure 41. W_r, V_r graph for onset-of-heading from backcross diallel set.

— $o = W_r, V_r$ intercepts
at Ellerslie
---- $\Delta = W_r, V_r$ intercepts
at Parkland

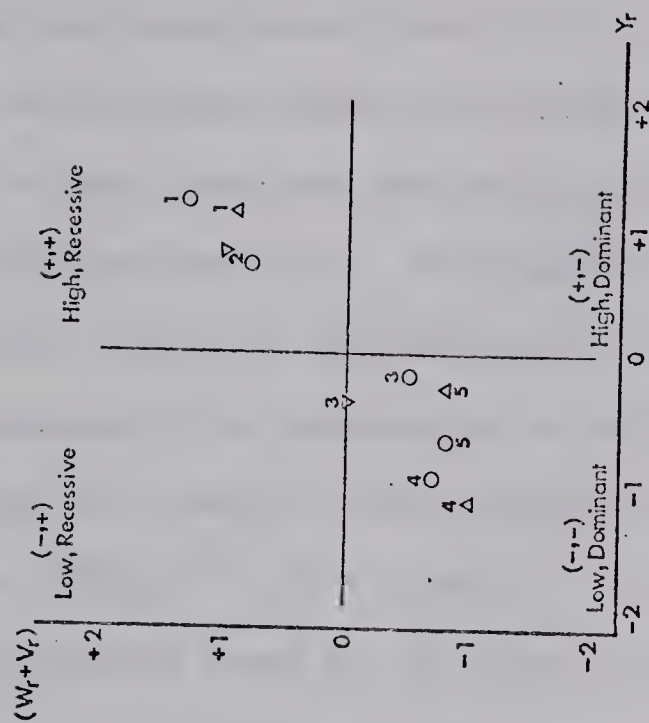


Figure 42. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for onset-of-heading from backcross diallel set.

$o = Y_r, [W_r + V_r]$ intercepts
at Ellerslie
 $\Delta = Y_r, [W_r + V_r]$ intercepts
at Parkland

of variation were significant (Table 59) for onset-of-heading. The mean degree of dominance (Table 60) and the regression of W_r upon V_r (Figure 41) at both locations show that onset-of-heading is inherited as a partially dominant trait. The proportion of positive to negative alleles at loci exhibiting dominance in the parents is approximately 0.25 and consequently the parents may be assumed to have equal proportions of genes with positive and negative effects respectively. The estimates of $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F] > 1$ for both locations suggest that dominant genes are in excess in the parents. Moreover, since h^2/H_2 is 1.2 for Ellerslie and 2.5 for Parkland, at least one and at least two groups of genes, respectively, are showing dominance in regard to the expression of the character. The correlation coefficient between Y_r and $(W_r + V_r)$ at both locations is 0.9, indicating that the genes for early heading are mostly dominant. The parents Marquis and Inia at Ellerslie and Chinook and Ciano at Parkland are the most highly recessive and highly dominant ones (Figure 41). The standardized deviation graph of Figure 42 categorized the late heading parents as recessives (Marquis and Chinook, in the +,+ quadrant) and the early parents as dominants (Khush-hal, Ciano and Inia, in the -,- quadrant) for both locations. Heritability estimates of 102.75% at Ellerslie and 75.27% at Parkland show that the character is highly heritable and fairly stable over the environmental fluctuations.

Only F and E for final heading were not significant at Ellerslie (Table 59). The character is partially dominant in its inheritance since $(H_1 \div D)^{1/2} < 1$ (see also Figure 43). Table 57 shows $W_r - V_r$

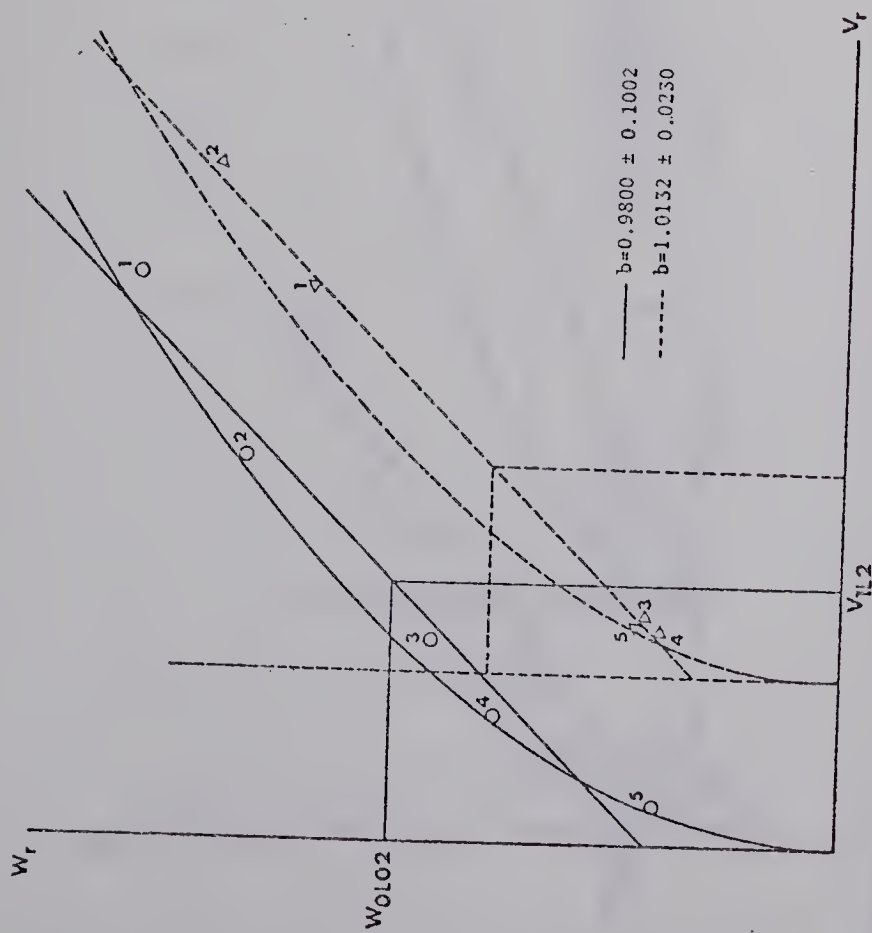


Figure 43. W_r , V_r graph for final heading from backcross diallel set.

— $o = W_r$, V_r intercepts
at Ellerslie
--- $\Delta = W_r$, V_r intercepts
at Parkland

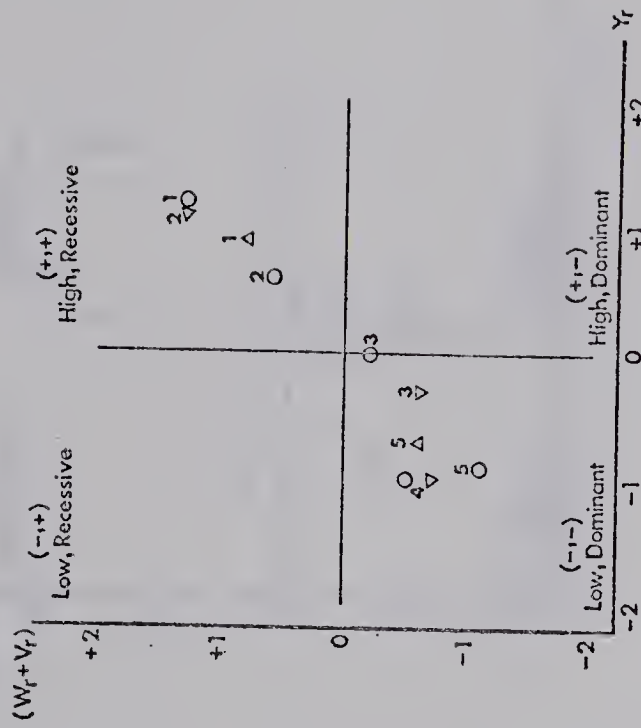


Figure 44. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for final heading from backcross diallel set.

$o = Y_r$, $[W_r + V_r]$ intercepts
at Ellerslie
 $\Delta = Y_r$, $[W_r + V_r]$ intercepts
at Parkland

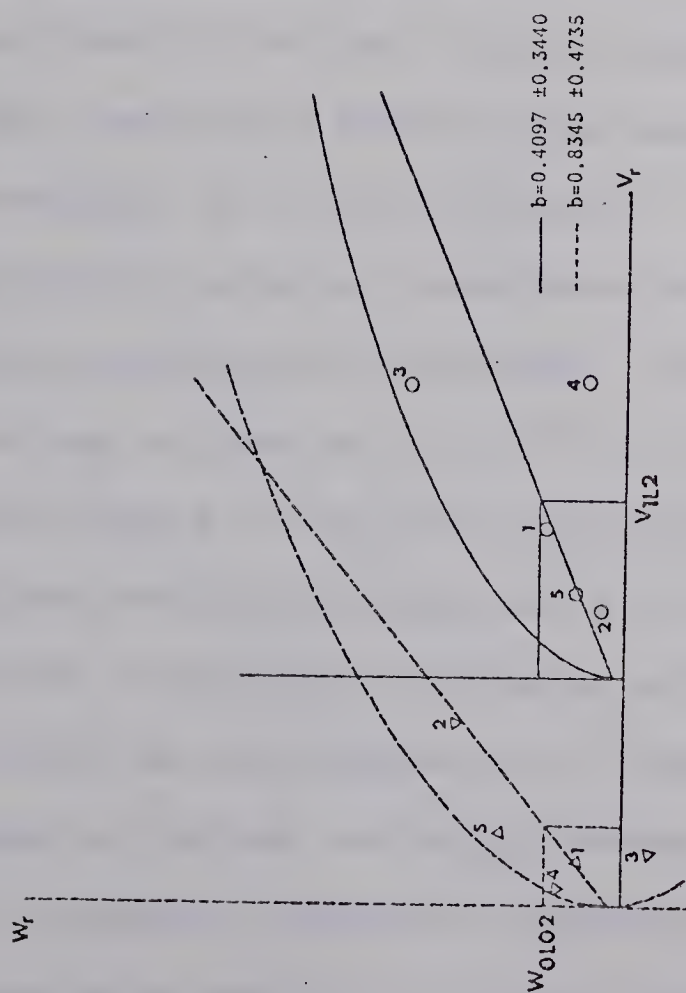


Figure 45. W_r, V_r graph for heading-span from backcross diallel set.

— $\circ = W_r, V_r$ intercepts
at Ellerslie
--- $\Delta = W_r, V_r$ intercepts
at Parkland

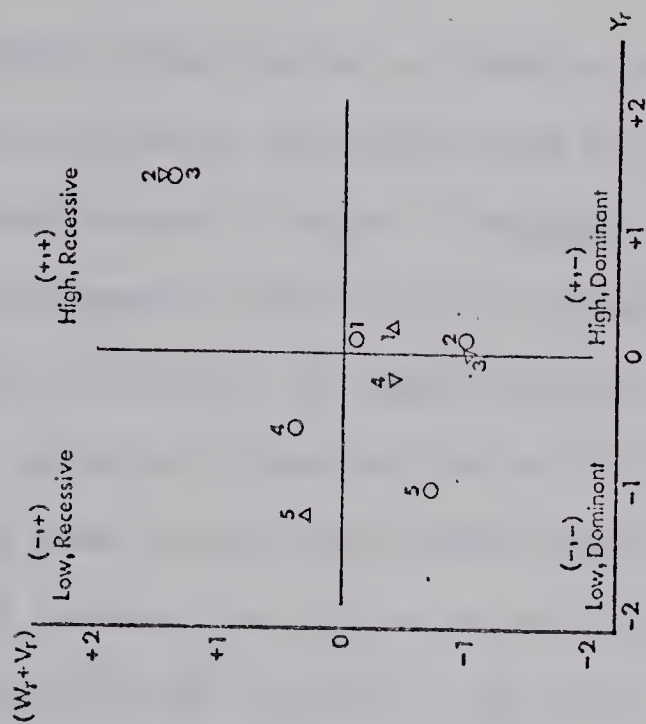


Figure 46. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for heading-span from backcross diallel set.

$\circ = Y_r, [W_r + V_r]$ intercepts
at Ellerslie
 $\Delta = Y_r, [W_r + V_r]$ intercepts
at Parkland

heterogeneity which can be ascribed to either non-allelic interaction, multiple allelism or correlated gene distribution. It could be ascertained from Figure 41 (onset-of-heading) and Figure 43 (final heading) that the regression line does not deviate significantly from the expected unit slope and the W_r, V_r graph does not appear to be distorted. Therefore the question of non-validity of any of the above mentioned conditions has been ignored. The general conclusions of the diallel analysis for final heading (see Tables 59, 60; Figures 43, 44) and heading-span (see Figure 45, 46) are similar to that for onset-of-heading except for changes in the ranking order of parents for their dominance.

For plant height, all components of genetic variation except D were non-significant at both locations. The $W_r - V_r$ heterogeneity at Parkland (Table 57) has been ignored, since the regression of W_r upon V_r is not significantly different from unity (Figure 47) and the W_r, V_r array-intercepts do not show distortion. Because of the non-significance of components of variation, interpretations of proportional estimates and genetic parameters are meaningless. However, the mean degree of dominance may be given as $(H_1 \div D)^{1/2} < 1$ indicating partial dominance (see also Figure 47). The correlation between the parental order of dominance and parental measurements is 0.32 at Ellerslie and -0.607 at Parkland. The positive correlation at Ellerslie indicates that genes for shortness are mostly dominant; the negative correlation at Parkland that genes for tallness are mostly dominant. The most highly recessive parent (+,+ quadrant, Figure 48) contributing to tallness at Ellerslie is Marquis, while Khush-hal is the most highly recessive parent at Parkland

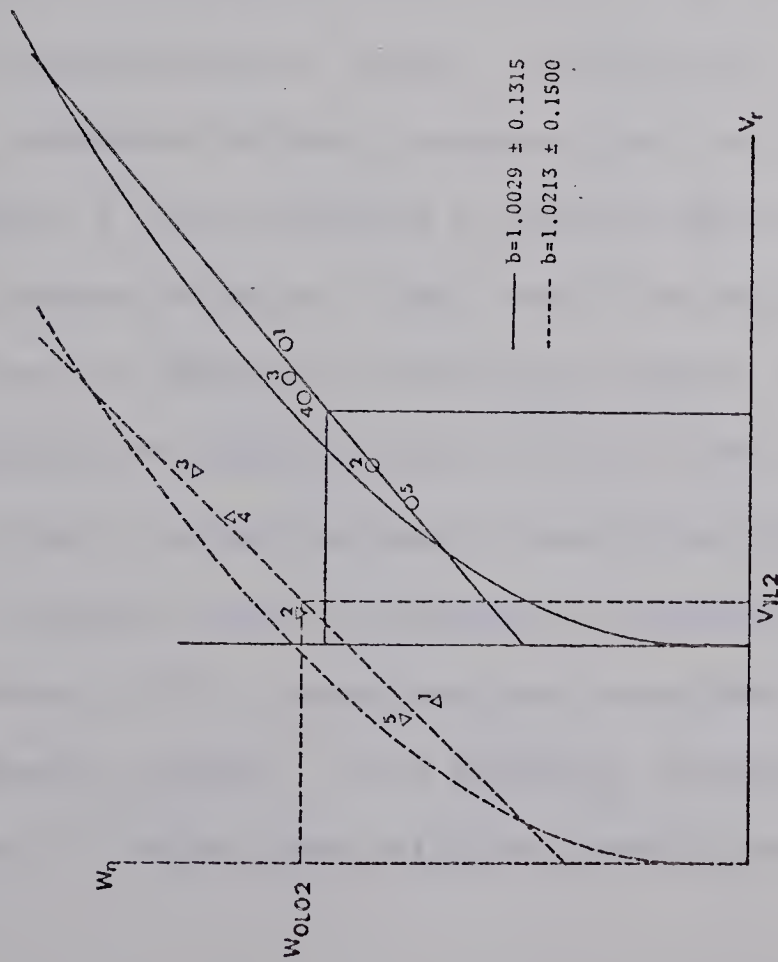


Figure 47. W_p , V_p graph for plant height from backcross diallel set.

— $\circ = W_p$, V_p intercepts at Ellerslie
 ---- $\Delta = W_p$, V_p intercepts at Parkland

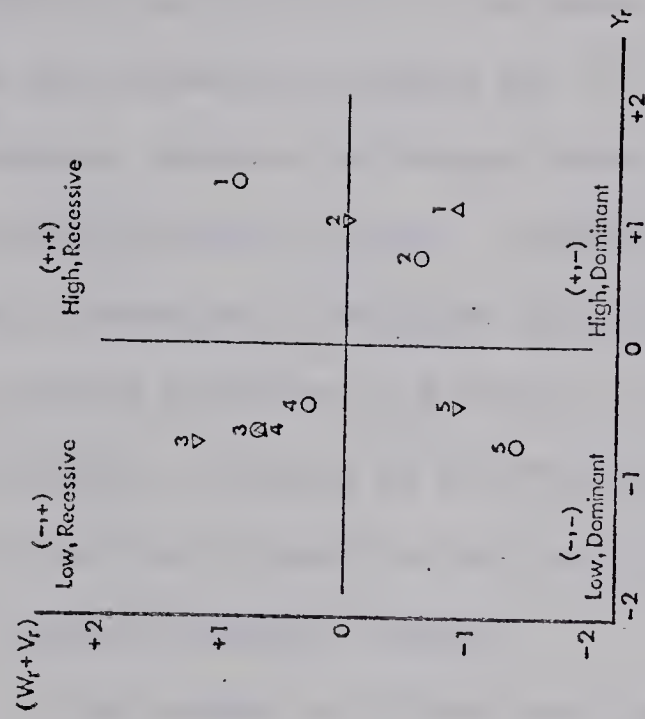


Figure 48. Standardized deviation graph of $[Y_p]$ and $[W_p + V_p]$ for plant height from backcross diallel set.

$\circ = Y_p$, $[W_p + V_p]$ intercepts at Ellerslie
 $\Delta = Y_p$, $[W_p + V_p]$ intercepts at Parkland

(-,+ quadrant) contributing to shortness. The most dominant parent, Inia, at both locations occupies the (-,-) quadrant and thus reflects its shortness. Marquis and Chinook show a discrepancy in dominance ranking order between locations. Chinook, highly dominant at Ellerslie had equal proportion of dominants and recessives at Parkland, while Marquis, highly recessive at Ellerslie is highly dominant at Parkland. The heritability estimates of 88.98% at Ellerslie and 84.77% at Parkland suggests that plant height, being highly heritable is quite stable with respect to environmental changes.

For number of tillers per plant, all components of variation except D and F are non-significant at Parkland. Consequently, proportional values discussed below may have a value only in showing trends and not definite conclusions. The same condition applies to the interpretation of graphs. At Ellerslie, $(H_1 \div D)^{1/2} \approx 1$, showing that dominance is nearly complete (see also Figure 49). The value of $(H_2/4H_1) = 0.204$ indicates a certain degree of asymmetry of positive and negative alleles at loci exhibiting dominance. the proportion of dominant to recessive genes in the parents (0.309), indicates a preponderance of recessive genes. Since $h^2/H_2 = 0.704$, probably at least one group of genes controls tillering capacity. The correlation between parental order of dominance and parental measurements at both locations is 0.9, suggesting that genes with low tillering capacity are mostly dominant. This situation is presented graphically in Figure 50, where almost all the parents at both locations occupy

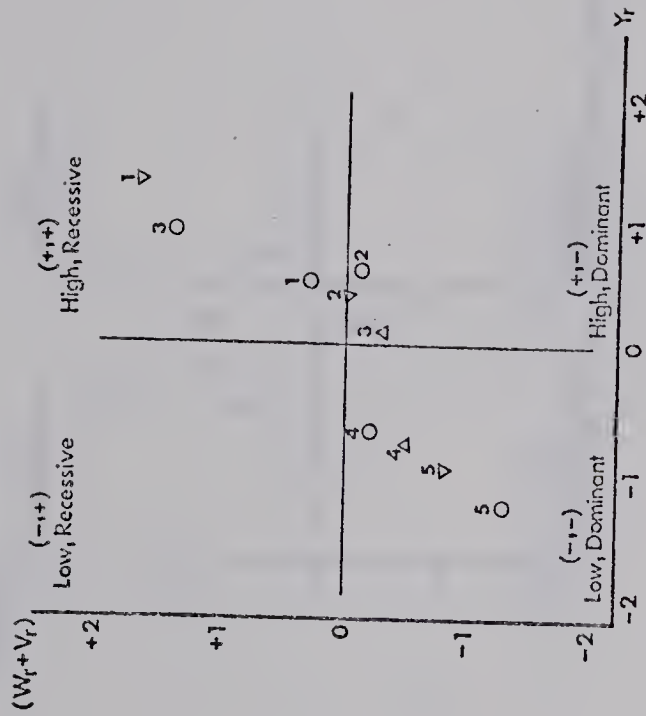


Figure 50. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of tillers per plant from backcross diallel set.
 $\circ = Y_r, [W_r + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r, [W_r + V_r]$ intercepts at Parkland

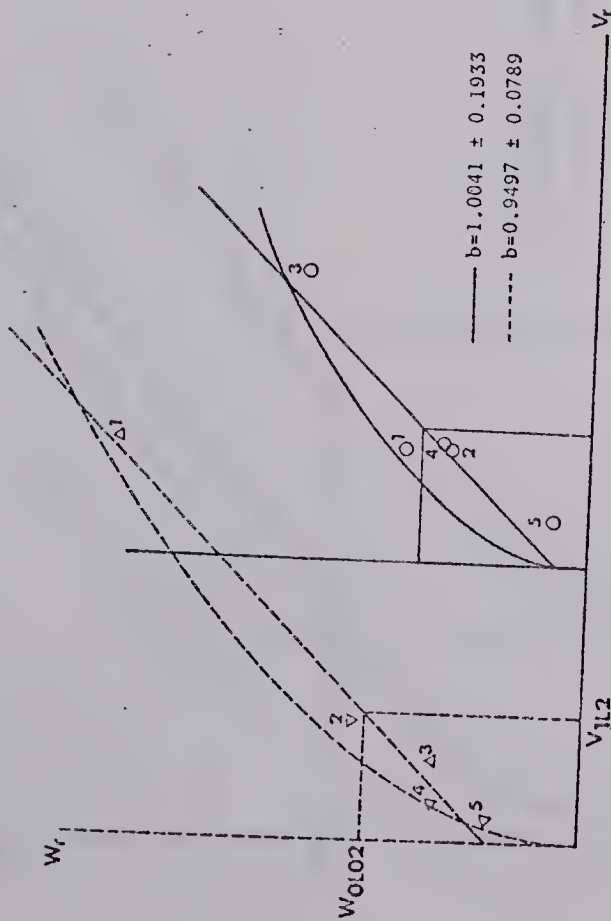


Figure 49. W_r, V_r graph for number of tillers per plant from backcross diallel set.
 — $\circ = W_r, V_r$ intercepts at Ellerslie
 --- $\Delta = W_r, V_r$ intercepts at Parkland

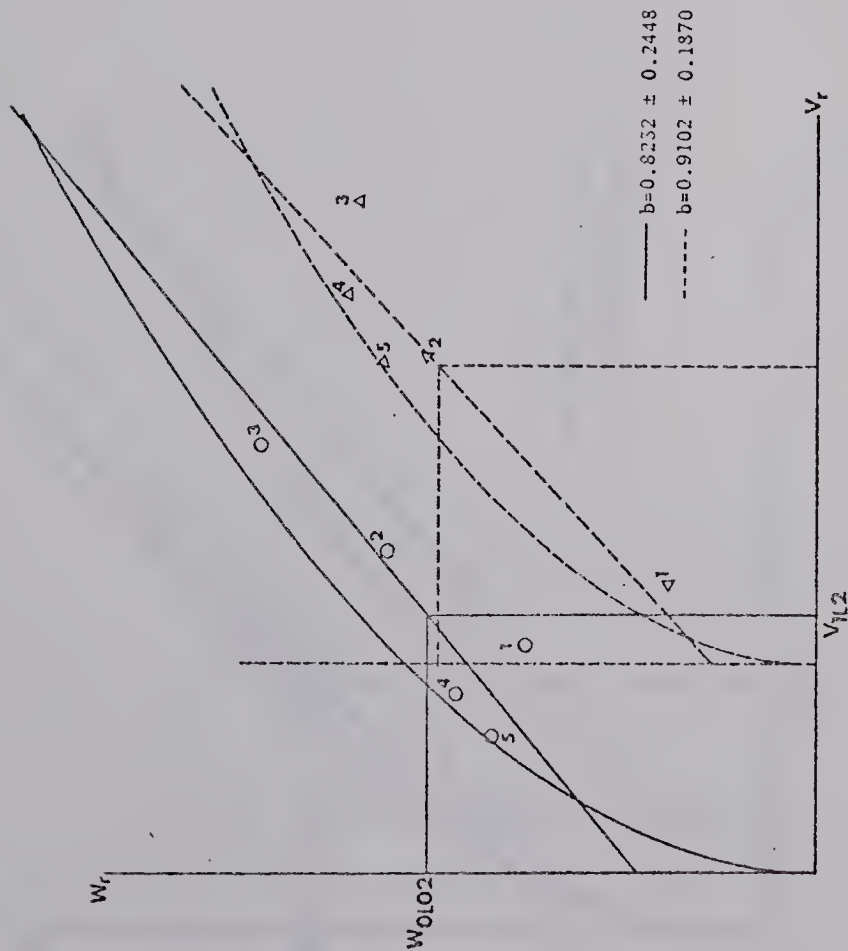


Figure 51. W_p , V_p graph for number of spikelets per spike from backcross diallel set.

— $o = W_p$, V_p intercepts
at Ellerslie
--- $\Delta = W_p$, V_p intercepts
at Parkland

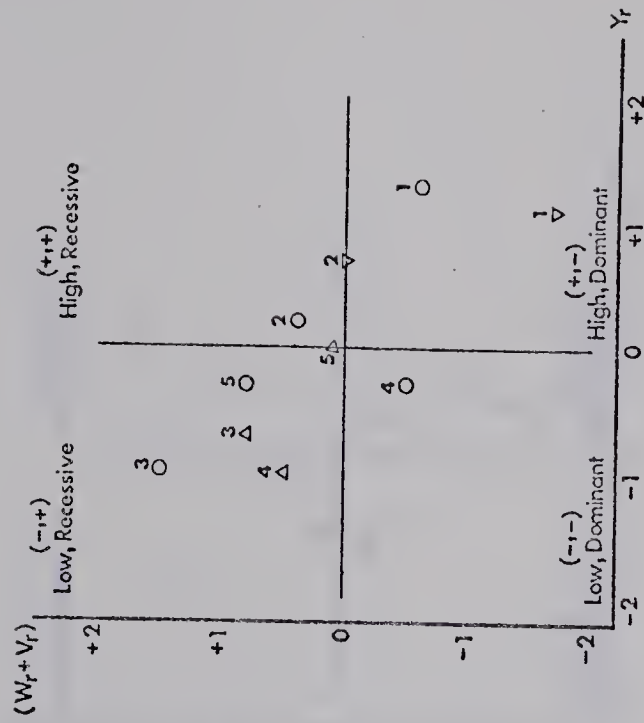


Figure 52. Standardized deviation graph of $[Y_p]$ and $[W_p + V_p]$ for number of spikelets per spike from backcross diallel set.

$o = Y_p$, $[W_p + V_p]$ intercepts
at Ellerslie
 $\Delta = Y_p$, $[W_p + V_p]$ intercepts
at Parkland

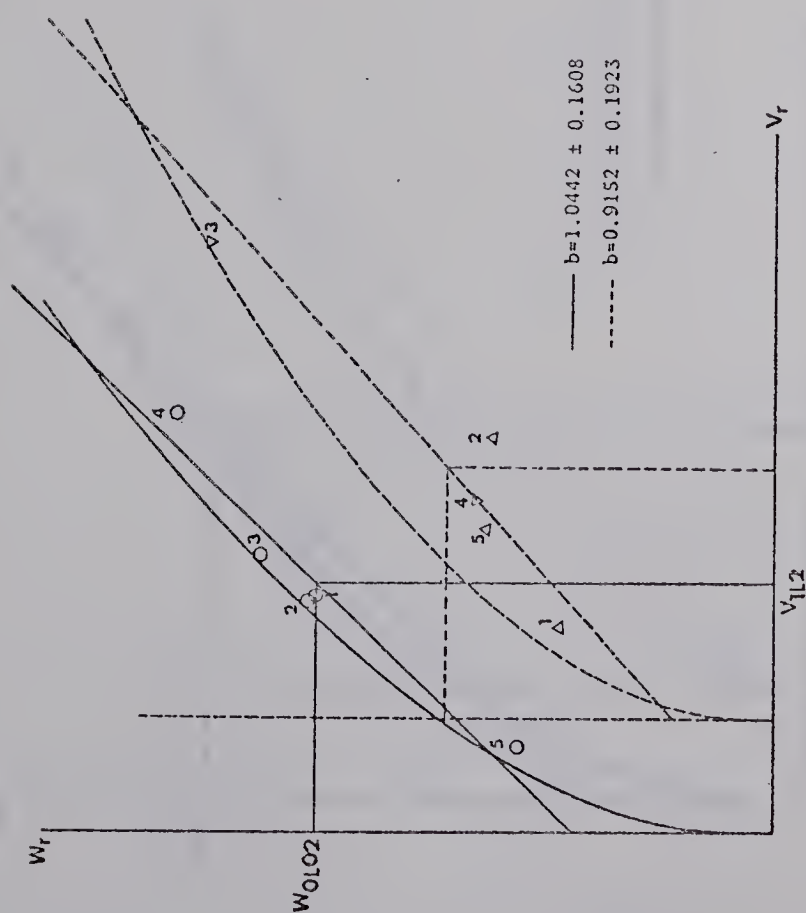


Figure 53. W_r, V_r graph for number of seeds per spike from backcross diallel set.

— $O = W_r, V_r$ intercepts
at Ellerslie
---- $\Delta = W_r, V_r$ intercepts
at Parkland

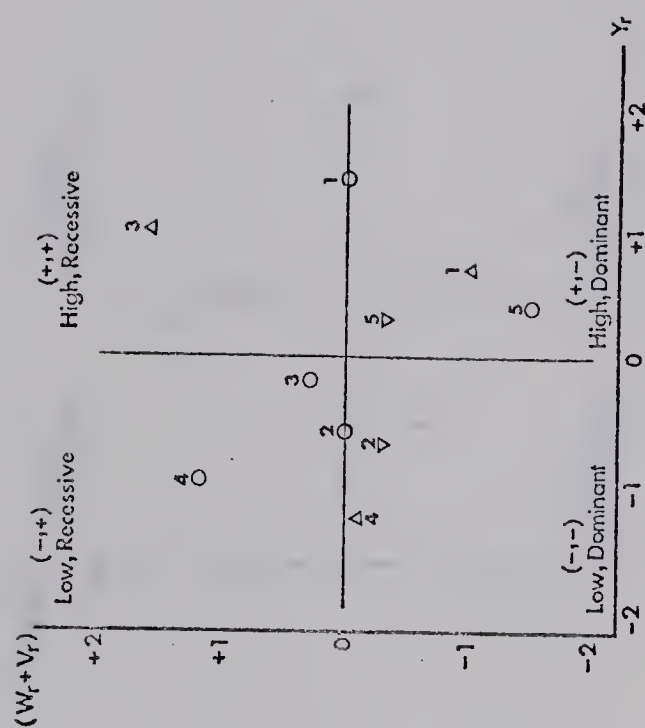


Figure 54. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of seeds per spike from backcross diallel set.

$O = Y_r, [W_r + V_r]$ intercepts
at Ellerslie
 $\Delta = Y_r, [W_r + V_r]$ intercepts
at Parkland

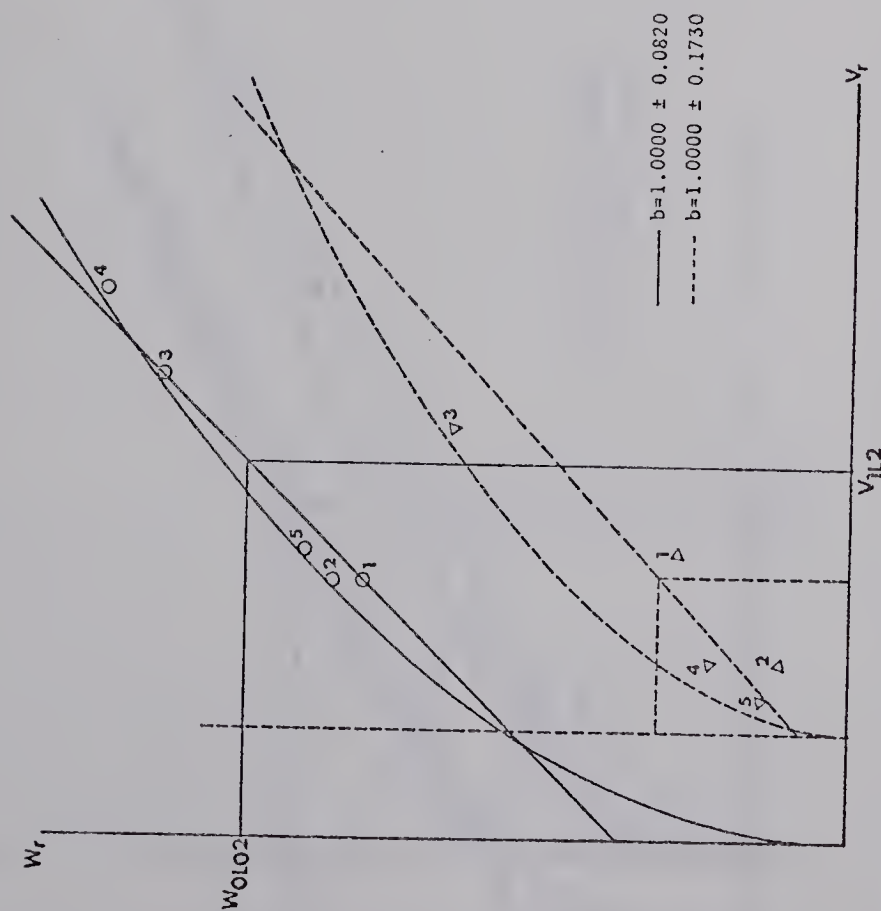


Figure 55. W_r, V_r graph for weight of seeds per spike from backcross diallel set.

— $\circ = W_r, V_r$ intercepts
at Ellerslie
--- $\Delta = W_r, V_r$ intercepts
at Parkland

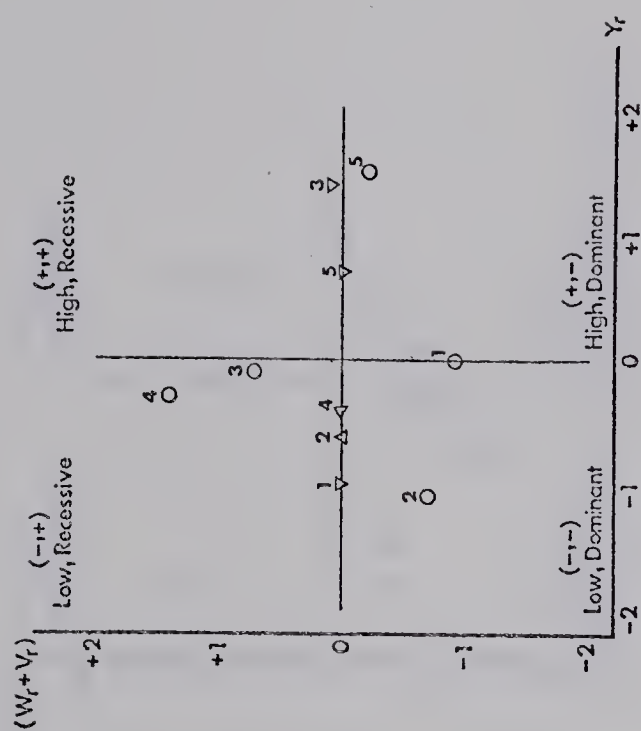


Figure 56. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for weight of seeds per spike from backcross diallel set.

$\circ = Y_r, [W_r + V_r]$ intercepts
at Ellerslie
 $\Delta = Y_r, [W_r + V_r]$ intercepts
at Parkland

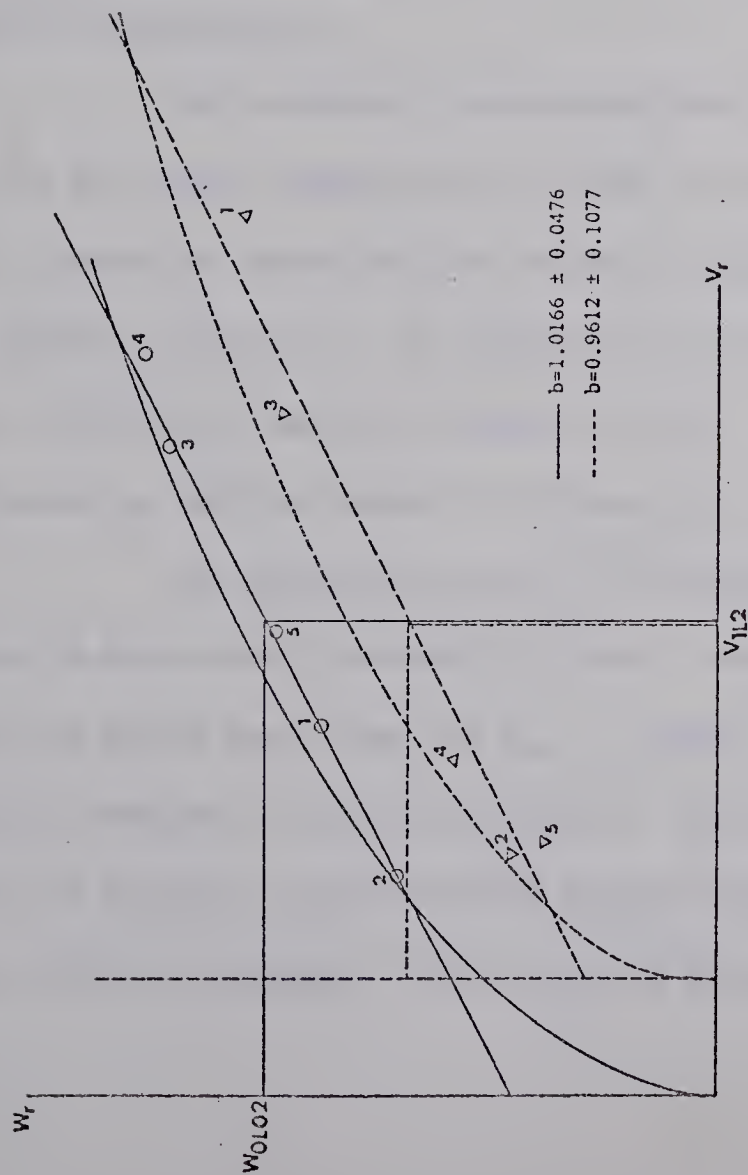


Figure 57. W_r, V_r graph for 1000-kernel weight from backcross diallel set.

— $o = W_r, V_r$ intercepts at Ellerslie

--- $\Delta = W_r, V_r$ intercepts at Parkland

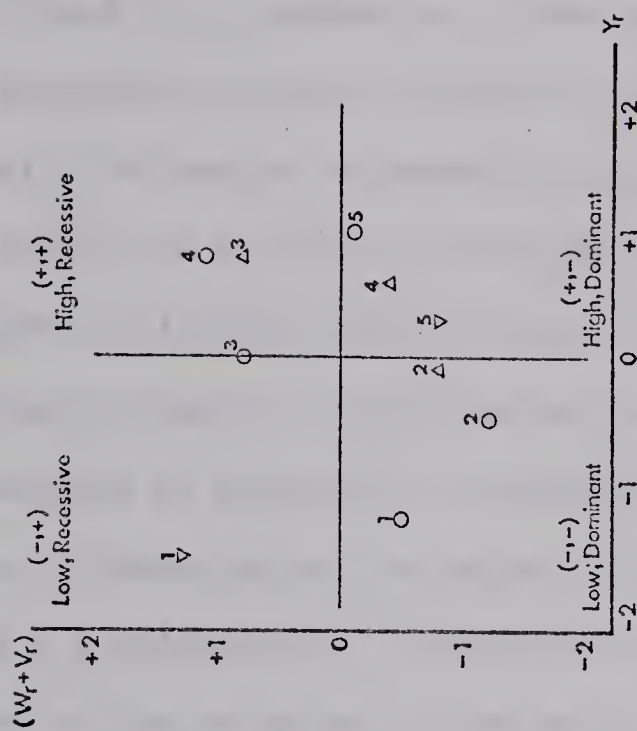


Figure 58. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for 1000-kernel weight from backcross diallel set.

$o = Y_r, [W_r + V_r]$ intercepts at Ellerslie

$\Delta = Y_r, [W_r + V_r]$ intercepts at Parkland

the (-,-) and (+,+) quadrants. Ciano and Inia, in the (-,-) quadrant, may be regarded as highly dominant for low tillering at both locations. Khush-hal at Ellerslie and Marquis at Parkland, in the (+,+) quadrant, may be said to be highly recessive for higher tillering. Chinook, with higher tillering capacity at both locations, shows more dominant than recessive genes at Ellerslie but equal proportions of dominants and recessives at Parkland. Only Khush-hal has changed its order of dominance between the two locations. Highly recessive at Ellerslie, it shows a preponderance of dominant genes at Parkland. Heritability values of 24.03% at Ellerslie and 83.79% at Parkland suggest that the heritability of tillering capacity is strongly influenced by environmental fluctuations.

The graphical interpretations of the results of Tables 59, 60 for other components of yield, are shown in Figures 51 - 58, (i.e. number of spikelets per spike, Figures 51, 52; number of seeds per spike, Figures 53, 54; weight of seeds per spike, Figures 55, 56; and 1000-kernel weight, Figures 57, 58). These may be explained in the same way as for number of tillers per plant.

For yield per plant, the components of variation in Table 59 were mostly non-significant. The overall picture of inheritance of yield seen from the W_r , V_r graph of Figure 59 is one of partial dominance at both locations. The correlations between parental order of dominance and parental measurements are 0.921 at Ellerslie and -0.436 at Parkland. These highly significant correlations indicate

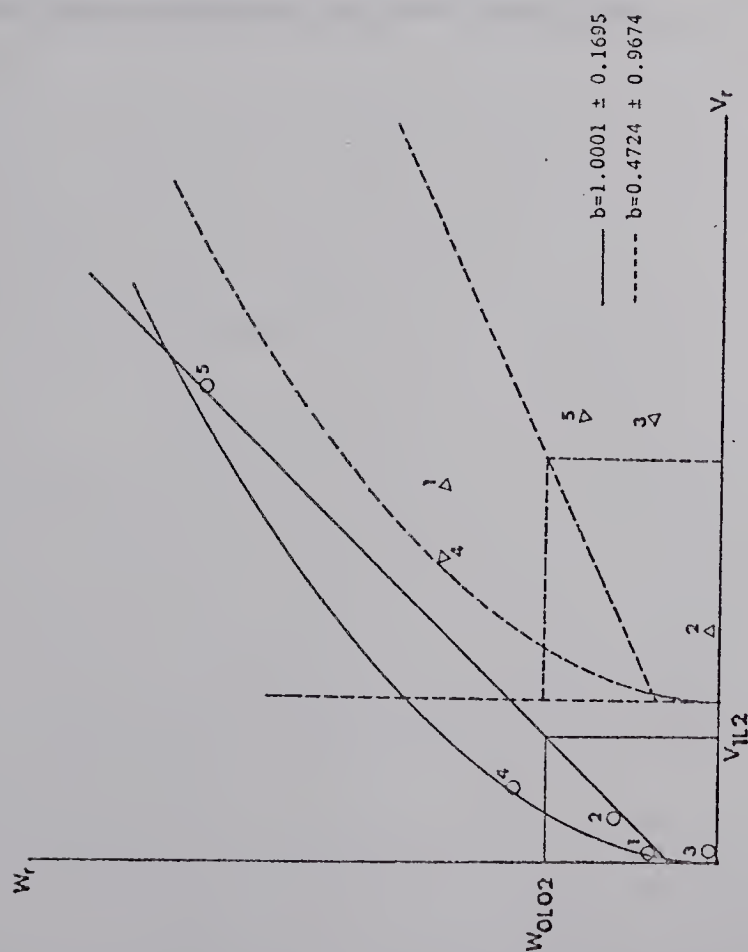


Figure 59. W_r , V_r graph for yield per plant from backcross diallel set.

— $o = W_r$, V_r intercepts at Ellerslie

--- $\Delta = W_r$, V_r intercepts at Parkland

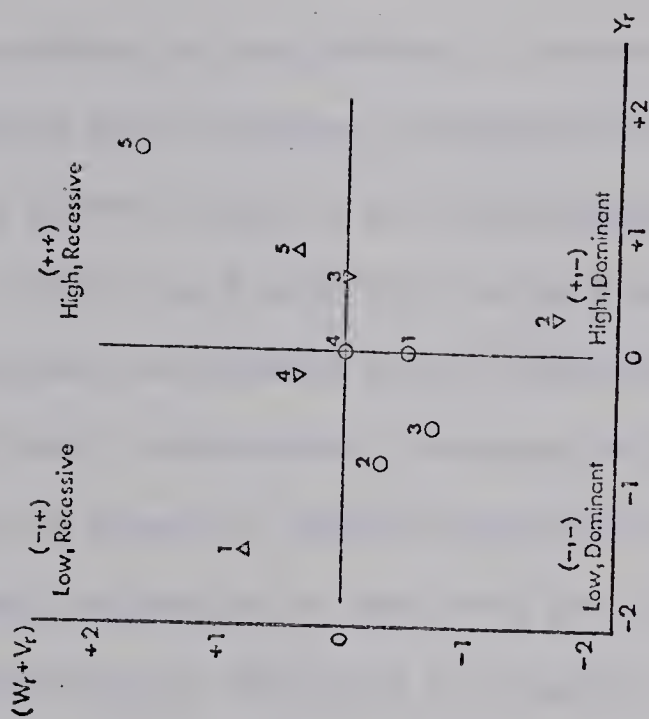


Figure 60. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for yield per plant from backcross diallel set.

$o = Y_r$, $[W_r + V_r]$ intercepts at Ellerslie

$\Delta = Y_r$, $[W_r + V_r]$ intercepts at Parkland

that the genes for low yield at Ellerslie are mostly dominant while at Parkland high yielding is dominant over low. The dominance ranking order of parents seems to be significantly different for the two locations. Thus, from Figure 59, Inia and Marquis are the most recessive and Khush-hal and Chinook are the most dominant parents at Ellerslie and Parkland, respectively. Marquis, highly recessive at Parkland contains an excess of dominant genes at Ellerslie, while Khus-hal, with equal proportion of dominants and recessives at Parkland shows a preponderance of dominants at Ellerslie. Ciano, with equal proportions of dominant and recessive genes at Ellerslie possesses an excess of recessive genes at Parkland. The heritability values of 65.67% at Ellerslie and 6.02% at Parkland reflect this instability of yield inheritance between the two locations.

ANALYSIS OF SELFED BACKCROSSES

In the absence of non-allelic interaction the expected statistics for the analysis of family means of the first selfed backcross generation are the same as those of F_3 generation crosses. The diallel table of selfed backcross family means, i.e., 'synthetic F_3 diallel table' was subjected to simple correlation analysis and the results are presented in Table 61. The following conclusions may be made from Table 61:

Onset-of-heading was positively correlated with final heading, plant height, number of spikelets per spike, number of seeds per spike at both locations and with number of tillers per plant at Parkland only. It was negatively correlated with weight of seeds per spike at Parkland and 1000-kernel weight at both locations. The negative correlation with weight of seeds per spike and 1000-kernel weight indicates that early maturing varieties produce higher yields and higher seed weights than the late maturing ones. Similar results were also obtained for F_1 , F_2 and backcross diallel data.

Plant height was positively correlated with number of tillers per plant and number of spikelets per spike at both locations and with number of seeds per spike at Ellerslie only. It was negatively correlated with weight of seeds per spike and 1000-kernel weight at both locations. Correlation with yield at both locations was not significant.

Number of tillers per plant was positively correlated with number of spikelets per spike and yield per plant at both locations

TABLE 61

Simple correlation coefficients between ten characters from a selfed backcross diallel set at two locations.

Character	2	3	4	5	6	7	8	9	10
1. Onset-of-heading	0.917** 0.842**	0.142 0.047	0.777** 0.818**	0.194 0.500**	0.534** 0.534**	0.346** 0.301**	-0.206 -0.288*	-0.643** -0.636**	-0.206 -0.162
2. Final heading	-	0.515** 0.578**	0.779** 0.771**	0.197 0.617**	0.445** 0.527**	0.316** 0.238*	-0.273* -0.347	-0.687** -0.656**	-0.307** -0.009
3. Heading-span		-	0.259* 0.191	0.055 0.390**	-0.081 0.169	-0.003 -0.011	-0.275* -0.204	-0.330** -0.254*	-0.349** 0.231*
4. Plant height			-	0.354** 0.511**	0.636** 0.588**	0.278* 0.155	-0.244* -0.465**	-0.606** -0.723**	0.016 -0.103
5. Number of tillers per plant				-	0.285* 0.428**	-0.056 0.239*	-0.034 -0.255	0.046 -0.536**	0.517** 0.253*
6. Number of spikelets per spike					-	0.619** 0.686**	0.212* 0.194	-0.412** -0.345**	0.252* 0.373**
7. Number of seeds per spike						-	0.695** 0.639**	-0.302** -0.061	0.126 0.409**
8. Weight of seeds per spike							-	0.526** 0.724**	0.442** 0.511**
9. 1000-kernel weight								-	0.418** 0.309**
10. Yield per plant									-

First reading under each column refers to Ellerslie and second to Parkland.

* Significant at 5% level

**Significant at 1% level

and with number of seeds per spike at Parkland. It was negatively correlated with 1000-kernel weight at Parkland. The correlation of tiller number with number of seeds per spike and 1000-kernel weight at Ellerslie and with weight of seeds per spike at both locations was not significant. A positive correlation with number of spikelets per spike, number of seeds per spike and yield per plant indicates a direct proportional relationship between tillering capacity and these characters, while negative correlation with 1000-kernel weight shows that plants with high tillering capacity tend to have a low kernel weight. The correlation coefficients for other components of yield, viz., number of spikelets per spike, number of seeds per spike and 1000-kernel weight among themselves and with heading dates have a similar interpretation.

Yield per plant was positively correlated with its components: 1000-kernel weight, weight of seeds per spike, number of seeds per spike, number of spikelets per spike and number of tillers per plant at both locations. The single exception was number of seeds per plant at Ellerslie. The positive correlation of yield with its components exhibits a direct proportional relationship of the former with the latter. Yield was negatively correlated with final heading and heading-span at both locations, indicating that the late heading entries are low yielding and vice versa. The negative correlation of yield with onset-of-heading was not significant at either location.

The results of the factor analysis are summarized in a varimax-rotated, five factor matrix in Table 62. 93% of the total

TABLE 62

Varimax rotated factor matrix for ten characters
from a selfed backcross diallel set at two locations.

Character	Communality	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5
Onset-of-heading	0.982 0.899	0.977 0.905	0.057 0.135	-0.034 0.193	-0.025 -0.005	0.147 -0.159
Final heading	0.985 0.956	0.908 0.786	0.036 0.078	-0.045 0.241	0.364 0.520	0.157 -0.065
Heading-span	0.986 0.991	0.163 0.086	-0.078 -0.057	-0.063 0.159	0.973 0.970	0.054 0.122
Plant height	0.850 0.924	0.787 0.924	0.010 -0.079	0.266 0.348	0.166 0.053	0.383 0.017
Number of tillers per plant	0.877 0.898	0.246 0.344	-0.120 0.079	0.889 0.817	0.100 0.227	0.030 0.234
Number of spikelets per spike	0.872 0.826	0.452 0.634	0.470 0.552	0.310 0.166	-0.158 0.058	0.572 0.296
Number of seeds per spike	0.955 0.978	0.251 0.199	0.895 0.953	-0.060 0.121	0.030 -0.011	0.293 0.122
Weight of seeds per spike	0.995 0.964	-0.206 -0.325	0.899 0.749	0.138 -0.389	-0.146 -0.112	-0.332 0.366
1000-kernel weight	0.939 0.902	-0.534 -0.581	0.126 0.115	0.261 -0.617	-0.204 -0.139	-0.727 0.388
Yield per plant	0.869 0.946	-0.232 -0.086	0.281 0.298	0.817 0.085	-0.261 0.140	-0.018 0.908
Percent of total Variability explained	93.095 92.841	31.338 33.077	19.500 19.144	17.231 14.301	12.604 13.203	12.421 13.115

First reading under each column refers to Ellerslie and second to Parkland.

variability present in the data for all the characters considered was explained by these factors at both locations.

The first factor was termed *lateness*. It carried highest loadings for onset-of-heading and final heading at both locations. Weight of seeds per spike, 1000-kernel weight and yield per plant were negative contributors to *lateness*. Of the remaining characters, the highest contributor to *lateness* was plant height at both locations. This confirms the results of the earlier F_1 , F_2 and backcross diallel factor analyses. *Lateness* explained 31.33% and 33.07% of the total variability at Ellerslie and Parkland respectively.

The second principal factor was termed *yielding~~f~~ability* ✓ since it carried the highest loadings on number of seeds per spike, weight of seeds per spike and number of spikelets per spike. As expected, yield per plant appreciably contributed to this factor. The contributions of onset-of-heading and final heading, though positive, were the lowest. Heading-span and plant height showed a negative effect on *yielding~~f~~ability*. ✓ The factor explained 19% of the variability present in the data at both locations.

Tillering~~f~~capacity was chosen as the third principal factor ✓ as it carried the highest loadings for number of tillers per plant at both locations. Yield per plant showed the highest contribution to *tillering~~f~~capacity* at Ellerslie but its effect at Parkland was very low. ✓ Other components of yield, viz., number of seeds per spike, weight of seeds per spike and 1000-kernel weight, contributed negatively or very slightly to *tillering~~f~~capacity* at both locations. A negative effect

TABLE 63

Estimates of general combining ability for five parental lines
used in selfed backcross diallel set for ten characters at two locations.

Character	Marquis	Chinook	Khush-hal	Ciano	Inia
Onset-of-heading	2.0733 2.3117	1.2483 1.5534	-0.5433 -0.6300	-1.6100 -2.3216	-0.0683 -0.9133
Final heading	2.8616 2.1917	1.4983 2.2334	-0.2433 -0.5500	-2.0183 -2.2250	-1.5183 -1.6500
Heading-span	0.1967 -0.1033	0.3717 0.6633	0.2550 0.0967	-0.4533 0.0967	-0.3700 -0.7533
Plant height	14.0397 12.5270	9.8603 12.5012	-8.6035 -8.7700	-6.1142 -7.7140	-9.1824 -8.5442
Number of tillers per plant	0.0554 0.7212	0.5642 0.7512	0.3819 0.3558	-0.0788 -0.7265	-0.9226 -1.1017
Number of spikelets per spike	0.7318 0.5099	0.1207 0.3313	-0.4789 -0.2941	-0.2321 -0.4894	-0.1415 -0.0577
Number of seeds per spike	3.7367 1.8352	-2.1908 -1.0805	-1.2477 0.4308	-1.6029 -1.8508	1.3047 0.6653
Weight of seeds per spike	0.0230 -0.0314	-0.1290 -0.0845	-0.0362 0.0607	-0.0017 -0.0282	0.1439 0.0834
1000-kernel weight	-2.3425 -2.0504	-1.1454 -1.0151	0.2488 0.9964	1.4072 0.9224	1.8379 1.1968
Yield per plant	-0.0471 0.5386	-0.8473 0.0681	-0.7653 0.3231	0.6451 -0.2341	1.0147 0.3815

First reading under each column refers to Ellerslie and second to Parkland.

was observed for onset-of-heading, final heading and heading-span at Ellerslie, but their effect at Parkland, though positive, was very low. *Tillering-capacity* explained 17.23% and 14.30% of the variability in the data at Ellerslie and Parkland.

The fourth principal component was chosen as *heading-span* because heading-span provided the highest contribution to this factor. It explained 12.6% and 13.2% of the variability at Ellerslie and Parkland. Yield per plant and its components had either a negative or a minimal effect on *heading-period*. This kind of response was also observed in the F_1 , F_2 and backcross factor analyses.

The fifth principal factor was named *low seed weight* at Ellerslie and *high yield* at Parkland because of the inconsistency in factor loadings between the two locations; 1000-kernel weight carrying maximum negative loading at Ellerslie and yield per plant maximum positive loading at Parkland. *Low seed weight* explained 12.421% and *high yield* 13.115% of the variability in the data at the respective locations. The contribution of yield and its components towards *low seed weight* at Ellerslie was expectedly low except number of spikelets per spike. On the other hand the contribution of yield components towards *high yield* at Parkland was definitely positive. *Low seed weight* was associated with earliness, as reflected by the factor loadings for heading data at the two locations.

Combining ability analysis

The results of the general combining ability analysis are presented in Table 63. For onset-of-heading Marquis was the highest

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from selfed backcross diallel set at two locations.

TABLE 64. Onset-of-heading

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia		
Marquis	-	0.4433 0.3217	-0.9317 -0.6616	-0.0733 0.6616	-1.1817 -0.9200	2.0733 2.3117	-0.1713 -0.2584
Chinook	-0.4583 -0.1667	-	-0.8566 -0.3617	-0.8733 -0.9617	-0.1066 -0.1617	1.2483 1.5534	-0.1058 -0.2239
Khush-hal	0.5417 0.3333	-0.2917 -0.5417	-	0.2933 0.4717	0.5183 0.0217	-0.5433 -0.6300	0.3626 -0.0689
Ciano	0.3333 0.5000	0.1250 0.2500	0.4167 -0.5000	-	0.5433 -0.3700	-1.6100 -2.3216	0.1134 0.2494
Inia	0.1667 -0.0417	-0.2500 -0.1250	0.0833 0.8750	-0.3750 0.1250	-	-1.1683 -0.9133	0.4859 0.0782

Reciprocal effects

TABLE 65. Final heading

Marquis	-	0.4517 0.9417	-0.6816 -1.4000	-0.2400 -0.5167	-0.8233 -0.9250	2.2816 2.1917	-0.1169 -0.4233
Chinook	-1.0417** -0.5833	-	-0.9817 -1.4833	-0.4983 -1.3500	0.8350 -1.2583	1.4983 2.2334	-0.0489 -0.1277
Khush-hal	0.5000 0.1250	-0.3333 -0.0833	-	0.3683 1.0167	-0.0483 0.8167	-0.2433 -0.5500	0.3592 0.9634
Ciano	0.6667* 0.5000	0.7083* 0.2917	0.7500** -0.3750	-	0.1433 0.4500	-2.0183 -2.2250	0.0303 0.6177
Inia	1.0833** 0.2500	-0.4583 0.0417	-0.2500 0.2500	-0.2500 0.0417	-	-1.5183 -1.6500	0.3491 0.6795

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level

**Significant at 1% level

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from selfed backcross diallel set at two locations.

TABLE 66. Heading-span

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia		
Marquis	-	-0.0800 0.6200	0.2867 -0.6883	-0.1300 -1.1467	0.3700 -0.0050	0.1967 -0.1033	-0.1405 -0.4982
Chinook	-0.6550 -0.4167	-	-0.2217 -1.1217	-0.2783 -0.3717	0.8200 -1.1467	0.3717 0.6633	-0.1304 -0.3700
Khush-hal	-0.0417 -0.1250	-0.0417 0.4583	-	0.0200 0.5283	-0.5217 0.7950	0.0088 -0.1887	-0.0968 0.0821
Ciano	0.3333 0.0	0.5833 0.0417	0.2917 0.1250	-	-0.3550 0.8367	-0.4533 0.0967	-0.1089 0.0822
Inia	0.9167** 0.2917	-0.2083 0.2500	-0.3333 -0.6250	0.1250 -0.0883	-	-0.3700 -0.7533	0.2620 0.3871

TABLE 67. Plant height

Marquis	-	-0.9476 -0.2017	0.7593 2.1257	2.0884 2.3297	-3.1655 -4.4209	14.0397 12.5270	-2.9557 -3.8799
Chinook	-0.8675 1.6562	-	-1.0681 0.3258	0.9945 0.1680	5.5803 2.0856	9.8603 12.5012	-2.6564 3.8664
Khush-hal	2.7857 2.7450	2.4108 1.8100	-	0.4511 2.1056	0.6493 -0.9884	-8.6035 -8.7700	-2.3832 -2.3383
Ciano	5.4176** 5.5917**	0.8667 2.7682	-0.8083 0.1045	-	-2.4269 -1.6792	-6.1142 -7.7160	-1.1045 -0.5836
Inia	4.6572** 3.6565*	4.8180** 3.6762*	2.4962 -0.8220	0.4758 -0.1612	-	-9.1824 -8.5442	12.8684 5.3504

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level

**Significant at 1% level

in GCA and Ciano was the lowest. Marquis at Ellerslie and Chinook at Parkland ranked first for final heading while Ciano at both locations ranked last. For heading-span, Chinook showed the highest GCA and Inia the lowest at both locations. Marquis was the best combiner for plant height at both locations, while Inia at Ellerslie and Khush-hal at Parkland were the poorest. Chinook showed the highest GCA for number of tillers per plant at both locations and Inia was the lowest. Interpretations of GCA's for number of spikelets per spike, number of seeds per spike, weight of seeds per spike and 1000-kernel weight may be made in the same way. For yield per plant, Inia at Ellerslie and Marquis at Parkland had the highest GCA while Chinook at Ellerslie and Ciano at Parkland were the poorest.

The estimates of specific combining abilities, reciprocal effects and variances for general and specific combining abilities for onset-of-heading, final heading and heading-span are presented in Tables 64, 65 and 66. For onset-of-heading, cross (CxI) at Ellerslie and (MxC) at Parkland had the highest SCA while cross (MxI) at Ellerslie and (CHxC) at Parkland scored lowest. The best hybrid (CxI) at Ellerslie had parents with the lowest GCA's at both locations while the worst (MxI) and (CHxC) had one parent Marquis and Chinook which showed the highest GCA's at both locations. The variances for GCA were greater than those for SCA in all cases and the reciprocal effects were not significant. Interpretations for final heading (Table 65) and heading-span (Table 66) may be made in the same way.

For plant height (Table 67), hybrid (CHxI) at both locations

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from slefed backcross diallel set at two locations.

TABLE 68. Number of tillers per plant

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia		
Marquis	-	-0.2510 -0.1161	-0.7515 -0.5486	0.5171 -0.6927	0.2983 -1.0161	-0.1926 0.3487	-0.4891 -0.4286
Chinook	-0.8792 0.1237	-	-0.0109 -0.7988	1.0864 0.2752	-0.1939 0.6594	0.1227 0.3928	-0.4681 -0.4241
Khush-hal	-0.1787 -0.6792	-0.6125 -0.4780	-	0.1419 0.7439	0.6200 0.4993	-0.0498 -0.0448	-0.3008 -0.1156
Ciano	0.5208 1.3028*	-0.4260 0.7470	0.3883 0.2823	-	-0.6341 -0.3619	-0.1894 0.3563	0.0001 -0.0590
Inia	-0.1833 -0.0542	0.3333 0.5690	0.4685 -0.2125	-0.0167 0.0857	-	0.6556 1.0423	-0.1848 0.1873

TABLE 69. Number of spikelets per spike

Marquis	-	0.0734 0.5629	0.0484 0.1757	0.2291 -0.0347	-0.1514 -0.0883	0.7318 0.5099	-0.0810 -0.0870
Chinook	-0.1043 0.2835	-	-0.0157 -0.0718	0.5060 -0.0863	-0.3085 0.1990	0.1207 0.3313	-0.0792 0.0186
Khush-hal	0.2930 0.2293	0.2042 0.0835	-	0.1958 0.3633	0.3165 0.0295	-0.4789 -0.2941	-0.0801 -0.0750
Ciano	0.5625* 0.4038	-0.0867 0.4050	0.0905 0.4162	-	-0.1921 0.1860	-0.2321 -0.4894	0.0346 -0.0402
Inia	-0.1140 0.1040	0.3238 0.0657	0.1035 0.0598	-0.4457 -0.2070	-	-0.1415 -0.0577	0.0041 -0.0595

First reading under each column refers to Ellerslie and the second to Parkland.

*Significant at 5% level

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from selfed backcross diallel set at two locations.

TABLE 70. Number of seeds per spike

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano			
Marquis	-	-0.7567 1.1823	0.5266 0.3948	1.6680 1.0759	3.7367 1.8352	13.2888 2.9362	-1.6858 -1.0793
Chinook	-0.6193 0.3758	-	-1.5155 -0.9669	1.7828 0.2750	-2.1908 -1.0805	4.1253 0.7357	-1.4949 -0.6134
Khush-hal	2.2568* 0.4473	0.6265 1.2037	-	-0.6317 -0.6815	-1.2477 0.4308	0.8823 -0.2461	-0.8277 -0.7157
Ciano	3.6903** 1.9765	1.2785 2.0132	0.1728 1.6680	-	-1.6029 -1.8508	1.8950 2.7759	-0.4341 -0.5141
Inia	-0.1847 0.1222	1.2072 -0.5362	-1.7647 -0.0292	-1.2285 -1.0437	1.3047 0.6653	1.0280 0.0109	-0.6937 -0.0279

TABLE 71. Weight of seeds per spike

Marquis	-	0.0198 0.0547	0.0027 0.0141	0.0572 0.0700	-0.0088 0.0494	0.0230 -0.0314	-0.0013 -0.0005	-0.0045 -0.0039
Chinook	0.0158 0.0358	-	-0.0387 -0.0251	0.0596 0.0011	-0.0314 -0.0083	-0.1290 -0.0845	0.0148 0.0056	-0.0044 -0.0030
Khush-hal	0.0618 0.0115	0.0010 0.0585	-	-0.0354 -0.0536	0.0368 0.0111	-0.0362 0.0607	-0.0005 0.0021	-0.0040 -0.0037
Ciano	0.0885 0.0322	0.0058 0.0608	-0.0500 0.0683	-	-0.0179 0.0659	-0.0017 -0.0282	-0.0018 -0.0008	-0.0018 -0.0013
Inia	-0.0882 -0.0605	0.0082 -0.0293	-0.0368 -0.0732	-0.0763 -0.0942	-	0.1439 0.0834	0.0189 0.0054	-0.0036 -0.0016

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level

**Significant at 1% level

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from selfed backcross diallel set at two locations.

TABLE 72. 1000-kernel weight

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia		
Marquis	-	0.1205 0.3031	-0.4528 0.0634	-0.2338 0.5471	0.7582 1.7552	-2.3425 -2.0504	-1.1713 -0.9369
Chinook	0.6497 6.4662	-	0.4032 0.0455	-0.1392 -0.2633	-1.1356 -0.8131	-1.1454 -1.0151	-1.1665 -0.9063
Khush-hal	-0.2560 -0.0027	-0.3190 0.5133	-	-0.3410 0.5745	0.0372 0.2047	0.2448 0.9964	-1.0488 -0.9325
Ciano	-0.9073 -0.8827	-0.9833 -0.2765	-1.1687 0.1982	-	-0.8553 0.5392	1.4072 0.9224	-1.1070 -0.7040
Inia	-1.5043 -1.1452	-0.5807 -0.1232	0.6037 -1.6265	-0.5812 -1.2087	-	1.8379 1.1468	-0.3055 0.4212

TABLE 73. Yield per plant

Marquis	-	-0.7261 0.5455	-0.3666 0.4427	0.7549 0.1542	0.5342 0.1742	-0.0471 -0.5386	-0.5317 -0.5930
Chinook	-0.7872 0.9510	-	0.0090 -1.0145	2.2304 0.3140	-0.7179 0.4450	-0.8473 0.0681	-0.3559 -0.4939
Khush-hal	0.4678 0.0278	-0.4883 0.3863	-	0.2590 0.4008	0.3710 0.7432	-0.7653 0.3231	-0.4868 -0.1846
Ciano	-0.3572 0.7125	-0.6105 0.7283	0.1253 1.4295*	-	-1.7015 -0.5442	0.6451 -0.2341	1.3389 -0.4987
Inia	-0.1232 0.2093	-0.2025 0.5000	-0.0010 -0.4568	0.0565 -0.1675	-	1.0147 0.3815	0.7462 -0.2341

First reading under each column refers to Ellerslie and the second to Parkland.
*Significant at 5% level

ranked highest while (MxI) ranked lowest. One parent of (CHxI), Chinook, showed the second highest GCA and the other, Inia, the lowest GCA at both locations. Similarly one parent of (MxI), Marquis, showed the highest GCA and other parent, Inia, the lowest GCA at both locations. The variances for GCA were greater in all the cases than those for SCA, and the reciprocal effects were non-significant, except for (CxM), (IxM) and (IxCH) at both locations. These effects may be attributed to the female parents of the respective crosses, because of the positive sign appended to each effect.

For number of tillers per plant, (CHxC) at Ellerslie and (KxC) at Parkland scored highest for SCA while cross (MxK) at Ellerslie and (MxI) at Parkland scored lowest (Table 68). The highest scoring hybrids at both locations had one parent, Ciano, with the second lowest GCA, while the poorest hybrids had one parent, Marquis, scoring second highest for GCA at both locations. The variances for GCA were greater than those for SCA except for Khush-hal at both locations and for Marquis and Ciano at Ellerslie. The reciprocal effects were generally non-significant except for (CxM) at Parkland. The results of the specific combining ability analysis for number of spikelets per spike (Table 69), number of seeds per spike (Table 70), weight of seeds per spike (Table 71) and 1000-kernel weight (Table 72) may be interpreted in the same way. Respective changes in the relative positions of the parents and hybrids for their GCA's and SCA's may be pointed out accordingly.

For yield per plant (Table 73), (CHxC) at Ellerslie and (KxI) at Parkland ranked highest for SCA while cross (CxI) at Ellerslie

TABLE 74

Analysis of variance of general and specific combining ability
and reciprocal effects from selfed backcross diallel set at two locations.

Character	M.S. for GCA	M.S. for SCA	M.S. for Reciprocal effects	Error M.S.
D.F.	4	10	10	48
Onset-of-heading	25.2656** 35.9375**	1.5062** 1.0437*	0.2253 0.3587	0.2568 0.3877
Final heading	34.6875** 44.3750**	0.0500** 3.8562**	0.8927 0.1934	0.1753 0.6340
Heading-span	1.4606** 2.5920**	0.4038 1.9051	0.3882 0.1924	0.2107 0.7428
Plant height	1225.0937** 1306.5469**	13.5937** 13.6375*	19.2865** 16.0161**	4.4336 5.8198
Number of tillers per plant	3.3135** 7.3857**	0.7684 1.3497*	0.4297 0.6839	0.7332 0.6427
Number of spikelets per spike	2.1357** 1.7500**	0.2266 0.2414	0.1581 0.1404	0.1166 0.1306
Number of seeds per spike	61.4688** 21.4844**	3.6574 2.8805	5.4534* 2.7848	2.5252 1.6190
Weight of seeds per spike	0.0980** 0.0489**	0.0033 0.0095	0.0059 0.0066	0.0068 0.0059
1000-kernel weight	30.5469** 21.0039**	1.0941 2.0250	1.4095 1.3617	1.7574 1.4052
Yield per plant	6.3789** 1.4990	2.5621** 0.7430	0.3304 0.9333	0.7980 0.8897

First reading under each column refers to Ellerslie and second to Parkland.

* Significant at 5% level

**Significant at 1% level

and (CHxK) at Parkland ranked lowest. The best hybrid at Ellerslie had one parent (Chinook) with the lowest GCA for that location while the best hybrid (KxI) at Parkland had one parent (Khush-hal) with the second lowest GCA for that location. On the other hand, the poorest ranking hybrid (CxI) at Ellerslie had one parent, Inia, with the highest GCA for that location while the lowest scoring hybrid at Parkland had one parent (Chinook) with the second highest GCA for that location. Variances for GCA were larger than those for SCA except for Marquis at Ellerslie, Chinook, Khush-hal and Inia at Parkland, and Ciano at both locations. Only cross (IxK) at Parkland showed significant reciprocal effect which may be ascribed to Inia.

Analysis of variance of general and specific combining ability (Table 74) yielded significant mean squares for GCA for all characters except for plant height, number of tillers per plant and yield per plant at Parkland. Significance for SCA mean squares for onset-of-heading, final heading and plant height at both locations, and for yield per plant at Ellerslie show a relatively greater importance of SCA over GCA for these characters in the selection procedures of the breeding programmes.

Diallel cross analysis

The assumption of no differences between reciprocal crosses is tested in Table 75. Significance of the *c* component for plant height, number of seeds per spike and 1000-kernel weight at both locations and heading-span and weight of seeds per spike at Parkland indicates reciprocal

TABLE 75

Mean squares from the analysis of variance
of 5 x 5 selfed backcross diallel set for ten characters at two locations.

Source of variation	D.F.	Onset-of- heading	Final heading	Heading- span	Plant height	Number of tillers per plant	Number of spikelets per spike	Number of seeds per spike	Weight of seeds per spike	1000 kernel weight	Yield per plant
<i>a</i>	4	75.7813** 107.8125**	104.0781** 133.2812**	4.3818* 7.7773	3675.7500** 3919.7500**	9.9355 22.1445**	6.4014** 5.2451*	184.4062** 64.4688**	0.2940* 0.1468*	91.6405** 62.9531**	20.6309 4.5000
<i>b</i>	10	4.5812** 3.1750	3.1875** 11.5562**	1.2113 5.7148	40.8000* 40.9000	2.3090 4.0539	0.6820 0.7270	11.0250 8.6687	0.0099 0.0286	3.3000 6.0937	7.6695 2.2301
<i>b</i> ₁	1	14.8519 12.1002	6.5269 41.2552	0.6533 8.6700	25.4775 10.2661	2.0285 5.5196	1.4763 4.5690*	12.0519 19.1386	0.0001 0.0721	10.1405 10.3402	1.2529 5.1668
<i>b</i> ₂	4	2.5469 1.1406	2.3125 5.7969	1.2296 4.6844	22.5000 61.6094	1.4173 5.2782	0.8340 0.0742	10.5986 11.3848	0.0095 0.0482	2.4014 9.7090	6.3564 0.3721
<i>b</i> ₃	5	4.1375** 3.0000	3.1625** 10.2500**	1.3086** 5.9492**	58.2000* 30.6375*	3.0828* 2.7836**	0.4086 0.4867	11.1500 4.4373	0.0124 0.0044	2.6750 2.3750	10.0445 3.1320
<i>c</i>	4	0.6323 0.4510	2.4437 0.2865	0.8052 0.6625*	124.9277** 111.7065**	1.1638 2.3081	0.6298 0.9578	31.4601* 18.2904**	0.0241 0.0421**	6.2645** 6.9694*	0.5412 4.0802
<i>d</i>	6	0.7052 1.4927	2.8344 0.7094	1.4042 0.5201	13.1473 5.6094	1.3726 1.8806	0.3740 0.0632	6.2935 1.7307	0.0134 0.0049	2.8714 2.1623	1.2913 1.9465
Blocks x <i>a</i>	8	0.6094 1.5469	0.5313 2.9687	0.6566 5.7076	35.1484 26.2500	4.2524 3.4097	0.6206 0.8687	21.3906 11.5391	0.0553 0.0357	12.6406 7.2256	3.5356 5.3936
Blocks x <i>b</i>	20	1.1750 1.5375	0.6219 2.7594	0.7967 2.6783	11.6469 27.2594	1.7006 2.4264	0.4297 0.4600	6.4000 5.3156	0.0207 0.0241	5.1812 5.0729	2.6195 2.7584
Blocks x <i>b</i> ₁	2	7.9587 4.9004	1.1337 22.8079	3.9429 9.6037	35.3591 243.6152	0.8380 29.1593	0.9345 0.0720	28.6814 1.6645	0.0527 0.0982	1.9094 31.9250	2.5027 3.6281
Blocks x <i>b</i> ₂	8	1.4365 1.9155	0.7158 2.1284	1.3752 4.2928	11.5615 27.5938	3.3234 2.0946	0.5036 0.8376	6.4800 10.4980	0.0332 0.0398	9.9072 6.9990	5.2974 3.9131
Blocks x <i>b</i> ₃	10	0.4187 1.0375	0.6062 1.5125	0.0988 0.9535	10.7312 8.1187	0.6729 0.2590	0.3559 0.2363	4.7937 2.0875	0.0095 0.0065	2.2551 1.3609	0.7465 2.0207
Blocks x <i>c</i>	8	0.4682 0.7901	0.7219 0.5036	0.6130 0.1562	6.4503 5.2429	1.0612 0.9600	0.2022 0.1437	4.9007 1.2552	0.0101 0.0034	0.6612 1.3100	1.3497 1.8076
Blocks x <i>d</i>	12	0.3979 0.5323	0.2479 0.7042	0.3552 0.5399	6.2170 3.8175	2.4131 0.7633	0.2015 0.1323	2.2132 2.0795	0.0034 0.2048	3.5959 2.7544	1.9556 1.2823
Error	48	0.7687 1.1632	0.5299 1.9045	0.6324 2.2223	13.3400 17.5610	2.2025 1.3010	0.3665 0.3935	7.6019 4.8671	0.0204 0.0178	5.2758 4.2249	2.3846 2.6701

* Significant at 5% level

**Significant at 1% level

First reading under each column refers to Ellerslie and second to Parkland. Error D.F. comprises of block interaction with D.F. of (a+b+c+d). Each component has been tested against its own block interaction.

TABLE 76

Analysis of variance of $\bar{W}$, $\bar{V}$, $\bar{r}$
from selfed backcross diallel set for ten characters at two locations.

Character	Block M.S.	Entry M.S.	Error M.S.
Onset-of-heading	9.6481 3.6885	0.3595 0.5320	0.3829 0.2390
Final heading	0.6643 34.1073	0.1281 1.1282	0.1925 1.2708
Heading-span	3.3027 4.9299	1.7202 0.4529	0.6324 1.3684
Plant height	9667.6563 6449.6875	139.6562 166.1875	55.6016 194.0000
Number of tillers per plant	3.0344 2.8647	0.2479 0.4159	0.8126 0.5661
Number of spikelets per spike	1.0906 0.0202	0.0335 0.0494	0.0445 0.0294
Number of seeds per spike	236.2362 27.1869	9.8044 2.0460	15.9139 6.1681
Weight of seeds per spike	0.0020 0.0014	0.00 0.0001	0.00 0.0001
1000-kernel weight	158.9355 18.6483	1.5762 5.1193	2.7423 5.6779
Yield per plant	13.4454 0.0343	9.2316 0.1368	4.4105 0.8050

First reading under each column refers to Ellerslie and second to Parkland.

TABLE 77

Estimates of second degree statistics from selfed
backcross diallel set for ten characters at two locations.

Character	V_{OLO}	W_{OLO}	V_{OL3}	V_{1L3}	$(M_{L1} - M_{LO})^2$
Onset-of-heading	15.0000 15.7002	6.1531 7.4624	2.5312 3.5977	3.2941 4.1244	0.7921 0.6454
Final heading	16.9668 27.1514	7.6016 10.9432	3.4756 4.4463	4.0049 6.3744	0.3481 2.2001
Heading-span	0.5889 3.6111	0.2319 0.9279	0.1462 0.2593	0.3480 1.2118	0.0348 0.4624
Plant height	486.7744 518.4434	243.1029 257.2012	122.5254 130.6758	128.3232 137.4928	1.3588 0.5476
Number of tillers per plant	1.4343 5.4749	0.6890 1.8430	0.3313 0.7383	0.7159 1.4139	0.1031 0.2944
Number of spikelets per spike	1.2283 0.5749	0.4789 0.3149	0.2136 0.1750	0.3275 0.2965	0.0737 0.2436
Number of seeds per spike	28.9980 12.2275	12.8658 4.6342	6.1455 2.1465	7.9799 3.5906	0.6427 1.0207
Weight of seeds per spike	0.0384 0.0360	0.0189 0.0115	0.0098 0.0049	0.0115 0.0097	0.0003 0.0038
1000-kernel weight	16.7744 13.1670	7.1279 4.9039	3.0537 2.0977	3.6014 3.1123	0.5408 0.5517
Yield per plant	5.4558 0.8875	1.7342 0.3533	0.6680 0.1502	1.9697 0.5220	0.0668 0.2755

First reading under each column refers to Ellerslie and second to Parkland.

differences for these characters. Significance of the a for all characters except heading-span at Ellerslie, number of tillers per plant at Parkland and yield per plant at both locations indicates substantial differences among the parents. Significance of b for final heading at both locations and onset-of-heading and plant height at Ellerslie shows that dominance is present while b_1 for number of spikelets per spike at Ellerslie shows that dominance is directional. Analysis of $W_r - V_r$ (Table 76) indicates that other assumptions, viz., no non-allelic interaction, no multiple allelism and uncorrelated gene distribution, are valid for all characters at both locations.

After Hayman's (1954a) procedure of replacement of reciprocal crosses by their common means, diallel analysis for genetic components of variation was carried out. Estimates of second degree statistics are given in Table 77 and the genetic components of variation obtained from them are presented in Table 78. Significance of components of variation was tested as in the previous diallel analyses of F_1 , F_2 and backcross sets. The proportional values of the estimates of genetic parameters from Table 78 are given in Table 79.

The ratio $(H_1/D_1)^{1/2} < 1$ for onset-of-heading at both locations (Table 79) shows that dominance is partial (see also Figure 61). The estimate of $[H_2 \div 4H_1] = 0.21$ at Ellerslie and 0.24 at Parkland implies some asymmetry in numbers of positive and negative alleles at loci exhibiting dominance at Ellerslie and equal proportion of positive and negative effects at Parkland. The proportion of dominant to recessive genes in the parents is > 1 at both locations indicating thus

TABLE 78

Estimates of genetic components of variation
from selfed backcross diallel set for ten characters at two locations.

Character	D	F	H ₁	H ₂	h^2	E
Onset-of-heading	14.7431 ± 0.2183** 15.3126 ± 0.1216**	5.0792 ± 0.5453** 1.0837 ± 0.3037**	2.8960 ± 0.5895** 1.3386 ± 0.3282**	2.5377 ± 0.5347** 1.3319 ± 0.2978**	3.0042 ± 0.3610** 2.3336 ± 0.2010**	0.2569 ± 0.0891** 0.3876 ± 0.0496**
Final heading	16.7914 ± 0.1955** 26.5164 ± 0.5872**	3.3169 ± 0.4884** 9.7681 ± 1.4668**	2.1242 ± 0.5280** 7.2254 ± 1.5859**	1.7665 ± 0.4789** 6.4425 ± 1.4383**	1.2804 ± 0.3233** 8.3949 ± 0.9711**	0.1753 ± 0.0798** 0.6350 ± 0.2397**
Heading-span	0.3781 ± 0.1789 2.8684 ± 0.3616**	-0.0027 ± 0.4468 2.6196 ± 0.9034**	0.5054 ± 0.4831 2.8158 ± 0.9766**	0.3859 ± 0.4381 2.3245 ± 0.8858**	0.0045 ± 0.2958 1.3742 ± 0.5981**	0.3108 ± 0.0750** 0.7428 ± 0.1476**
Plant height	482.3408 ± 5.9120** 512.6233 ± 4.8412**	-4.1831 ± 14.7833 1.0982 ± 12.0934	20.1284 ± 15.9824 24.4779 ± 13.0743	18.3242 ± 14.4962 15.6281 ± 11.8585	2.5981 ± 9.7870 -1.5344 ± 8.0062	4.4336 ± 2.4160** 5.8199 ± 1.9764**
Number of tillers per plant	0.7006 ± 0.1946** 4.8319 ± 0.2060**	-0.4873 ± 0.4861 2.8062 ± 0.5145**	-0.0852 ± 0.5256 2.0868 ± 0.5562**	0.0710 ± 0.4767 1.4165 ± 0.5045**	-0.0368 ± 0.3218 0.7661 ± 0.3406	0.7337 ± 0.0795** 0.6429 ± 0.0841**
Number of spikelets per spike	1.1068 ± 0.0601** 0.4444 ± 0.0434**	0.3953 ± 0.1501* -0.2666 ± 0.1084	0.3072 ± 0.1632 0.1616 ± 0.1172	0.2130 ± 0.1472 0.2248 ± 0.1063	0.2372 ± 0.0994** 0.8911 ± 0.0718**	0.1215 ± 0.0245** 0.1305 ± 0.0177**
Number of seeds per spike	26.4694 ± 0.7975** 10.6086 ± 0.7635**	3.4934 ± 1.9922** 3.9757 ± 1.9072**	2.8798 ± 2.1538 3.8441 ± 2.0619	2.2802 ± 1.9535 2.5387 ± 1.8702	0.9525 ± 1.3189 3.0465 ± 1.2626**	2.5286 ± 0.3256** 1.6189 ± 0.3117**
Weight of seeds per spike	0.0316 ± 0.0009** 0.0301 ± 0.0025**	-0.0017 ± 0.0023 0.0190 ± 0.0062**	-0.0092 ± 0.0025** 0.0133 ± 0.0067**	-0.0070 ± 0.0022** 0.0072 ± 0.0061	-0.0043 ± 0.0015** 0.0116 ± 0.0041**	0.0068 ± 0.0004** 0.0059 ± 0.0010**
1000-kernel weight	15.0175 ± 0.3606** 11.7616 ± 0.7518**	2.9288 ± 0.9008** 5.0319 ± 1.8779**	-1.8999 ± 0.9739 2.3466 ± 2.0302	-1.3233 ± 0.8833 1.2478 ± 1.8414	1.0390 ± 0.5964 1.3076 ± 1.2432	1.7569 ± 0.1472** 1.4054 ± 0.3069**
Yield per plant	4.6583 ± 1.1859** -0.0021 ± 0.1412	3.0180 ± 2.9624 -0.7056 ± 0.3527	4.3245 ± 3.2027 -0.7503 ± 0.3814	3.5319 ± 2.9049 -0.2918 ± 0.3459	-0.2431 ± 1.9612 0.5329 ± 0.2335	0.7975 ± 0.4841** 0.8896 ± 0.0476**

First reading under each column refers to Ellerslie and second to Parkland.

* Significant at 5% level

**Significant at 1% level

TABLE 79

Proportional values of the estimates of genetic parameters
from selfed backcross diallel set for ten characters at two locations.

Character	$[H_1/D]^{1/2}$	$[H_2/4H_1]$	$\left[\frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F} \right]$	h^2/H_2	$r_{Y,W}^2$	$r_{Y,V}^2$	Heritability
Onset-of-heading	0.4432* 0.2957*	0.2119* 0.2487*	2.2715* 1.2719*	1.1839* 1.7521*	0.9161 0.6870		1.0850 0.8945
Final heading	0.3557* 0.5220*	0.2079* 0.2229*	1.7689* 2.0905*	0.7248* 1.3030*	0.7816 0.9245		1.0301 1.0001
Heading-span	1.1562 0.9908*	0.1909 0.2064*	0.9939 2.7079*	0.0116 0.5912*	-0.0581 0.7279		0.2186 0.4752
Plant height	0.2043 0.2185	0.2276 0.1596	0.9584 1.0099	0.1418 -0.0982	-0.4065 -0.6697		0.9198 0.9165
Number of tillers per plant	0.3488 0.6572*	-0.2083 0.1697*	0.0013 2.5834*	-0.5189 0.5408	-0.7486 0.6240		0.1735 0.7228
Number of spikelets per spike	0.5268 0.6031	0.1733 0.3477	2.0258 0.3357	1.1137 3.9638	-0.8852 -0.0175		0.7355 0.3186
Number of seeds per spike	0.3298 0.6020	0.1979 0.1651	1.5011 1.9039	0.4177 1.2000	-0.6535 -0.5060		0.7359 0.6257
Weight of seeds per spike	0.5392 0.6649*	0.1904 0.1357	0.6546 2.8052*	0.6502 1.6045	0.9431 -0.2946		0.6159 0.6270
1000-kernel weight	0.3557 0.4467	0.1741 0.1329	1.7554 2.8281	-0.7852 1.0479	0.3482 -0.8856		0.8722 0.8002
Yield per plant	0.9635 18.9020	0.2042 0.0972	2.0130 -0.7970	-0.0688 -1.8262	0.3272 -0.5945		0.5088 -0.0005

First reading under each column refers to Ellerslie and second to Parkland.

*Proportional values involving genetic components of variation significantly different from zero ($P < 0.05$)

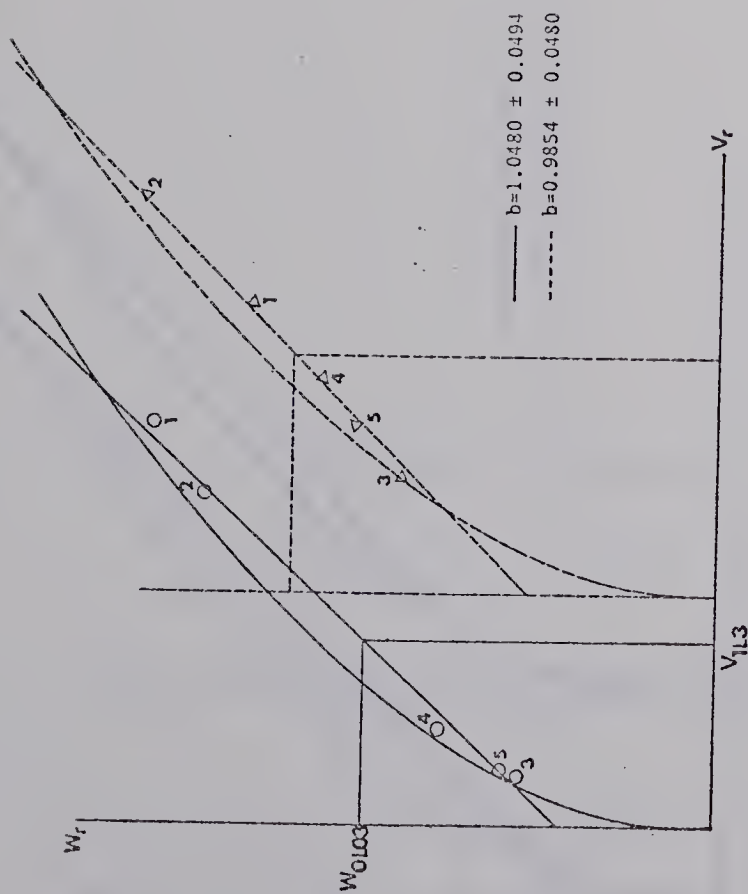


Figure 61. W_r , V_r graph for onset-of-heading from selfed backcross diallel set.

— $O = W_r$, V_r intercepts
at Ellerslie

--- $\Delta = W_r$, V_r intercepts
at Parkland

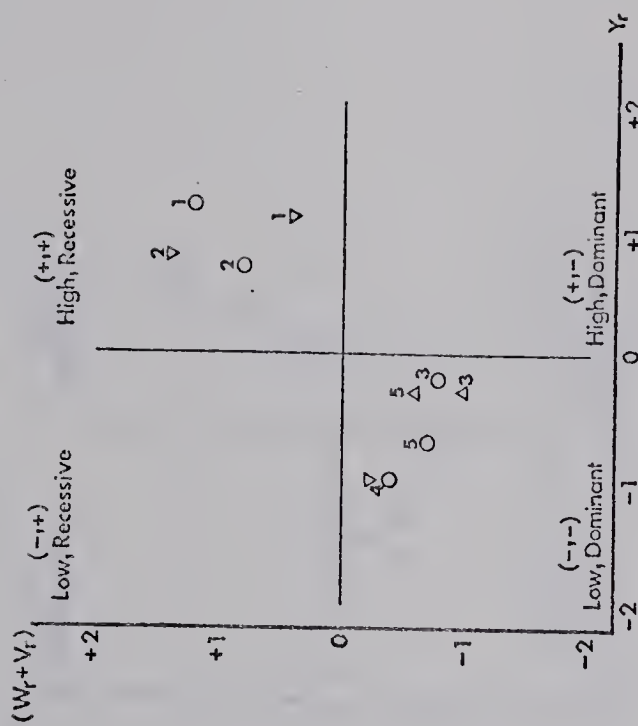


Figure 62. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for onset-of-heading from selfed backcross diallel set.

$O = Y_r$, $[W_r + V_r]$ intercepts
at Ellerslie

$\Delta = Y_r$, $[W_r + V_r]$ intercepts
at Parkland

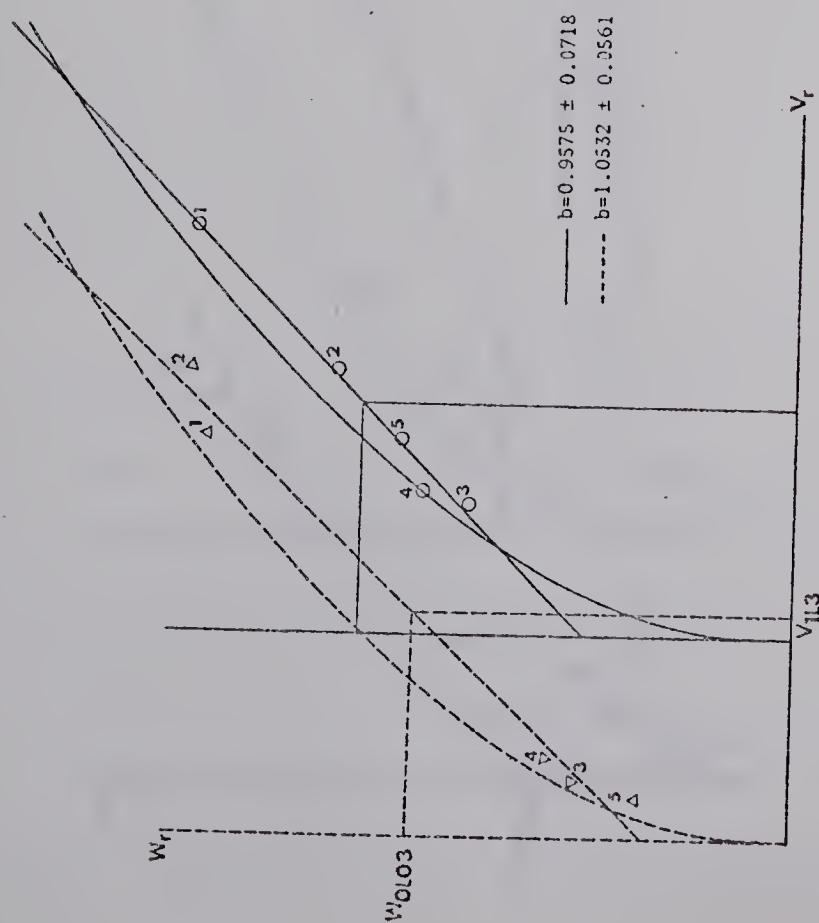


Figure 63. W_r, V_r graph for final heading from selfed backcross diallel set.

— $O = W_r, V_r$ intercepts
at Ellerslie
--- $\Delta = W_r, V_r$ intercepts
at Parkland

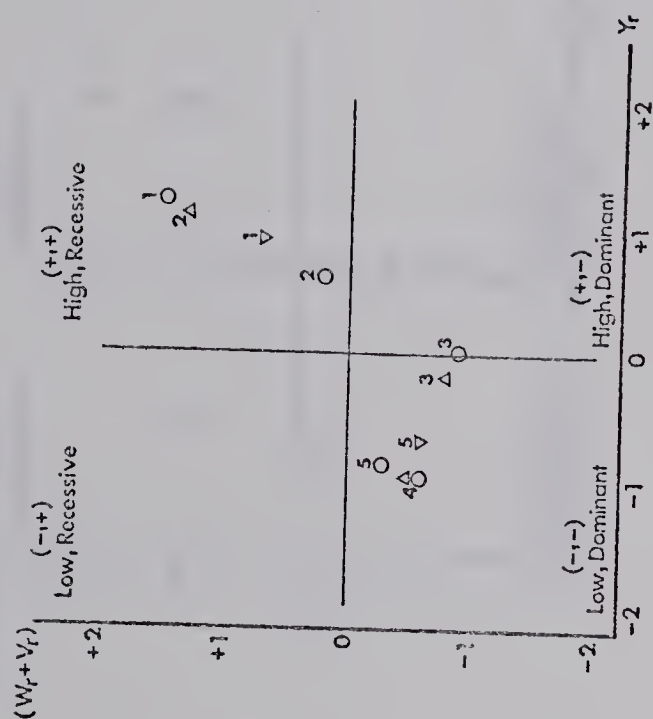


Figure 64. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for final heading from selfed backcross diallel set.

$O = Y_r, [W_r + V_r]$ intercepts
at Ellerslie
 $\Delta = Y_r, [W_r + V_r]$ intercepts
at Parkland

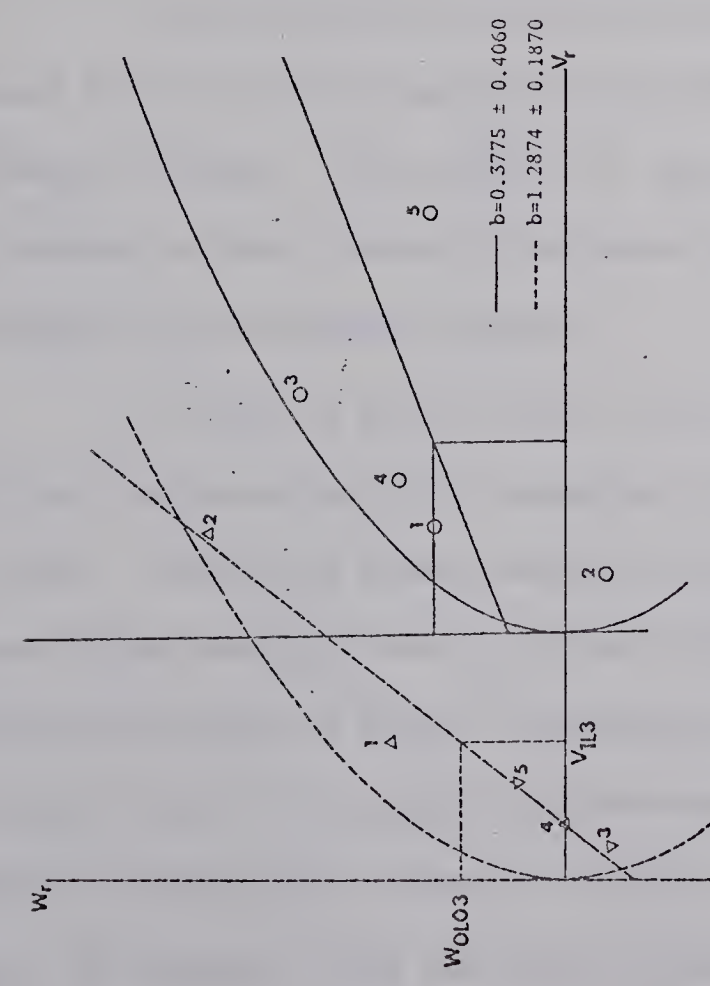


Figure 65. W_r, V_r graph for heading-span from selfed backcross diallel set.

— $o = W_r, V_r$ intercepts at Ellerslie

--- $\Delta = W_r, V_r$ intercepts at Parkland

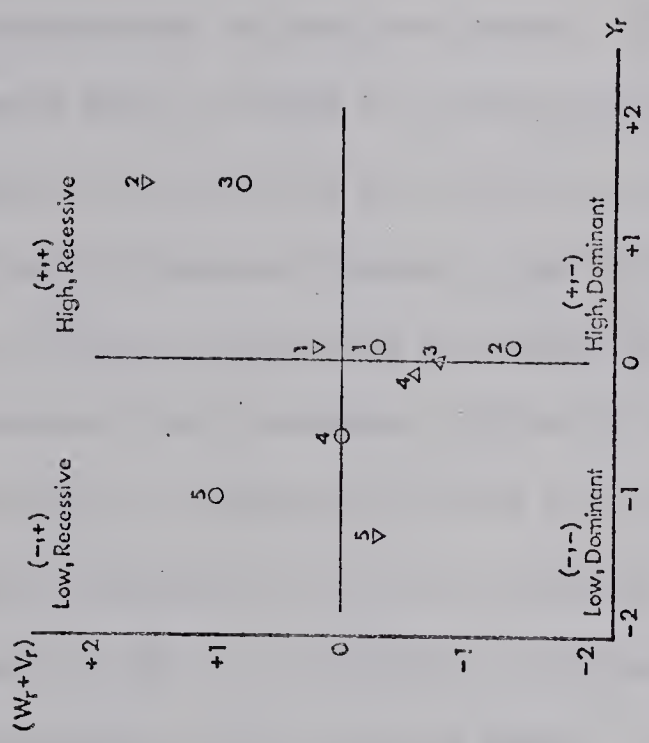


Figure 66. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for heading-span from selfed backcross diallel set.

$o = Y_r, [W_r + V_r]$ intercepts at Ellerslie

$\Delta = Y_r, [W_r + V_r]$ intercepts at Parkland

a preponderance of dominant genes. $[h^2/H_2] > 1$ at both locations suggests that at least two groups of genes exhibiting dominance contribute to the control of onset-of-heading. The coefficients of correlation between parental order of dominance and parental measurements (0.916 at Ellerslie and 0.687 at Parkland) indicate that earliness is dominant over lateness. Figure 61 shows that Marquis at Ellerslie and Chinook at Parkland are the most recessive parents while Khush-hal at both locations is the most dominant. Figure 62 places Marquis and Chinook in the (+,+) quadrant, indicating that lateness of these parents is associated with recessive genes. Khush-hal, Ciano and Inia occupy the (-,-) quadrant at both locations, suggesting that these parents are early maturing dominants.

The interpretations from Tables 78 and 79 for final heading (Figures 63, 64) and for heading-span (Figures 65, 66) may be made in the similar fashion. The changes in the relative position of the parents with respect to their order of dominance at the two locations could be attributed to environmental effects.

In case of plant height, the ratio of $[H_1/D]^{1/2} < 1$ at both locations indicates that the character is inherited as a partially dominant trait. Since all other components of variation, except D and E are non-significant at both locations (Table 78), the interpretation of proportional values of genetic parameters is meaningless. Figure 67 classifies Ciano at Ellerslie and Khush-hal at Parkland as the most recessive parents and Chinook as the most dominant at both locations. Figure 68 indicates that the most dominant parent (Chinook) at both

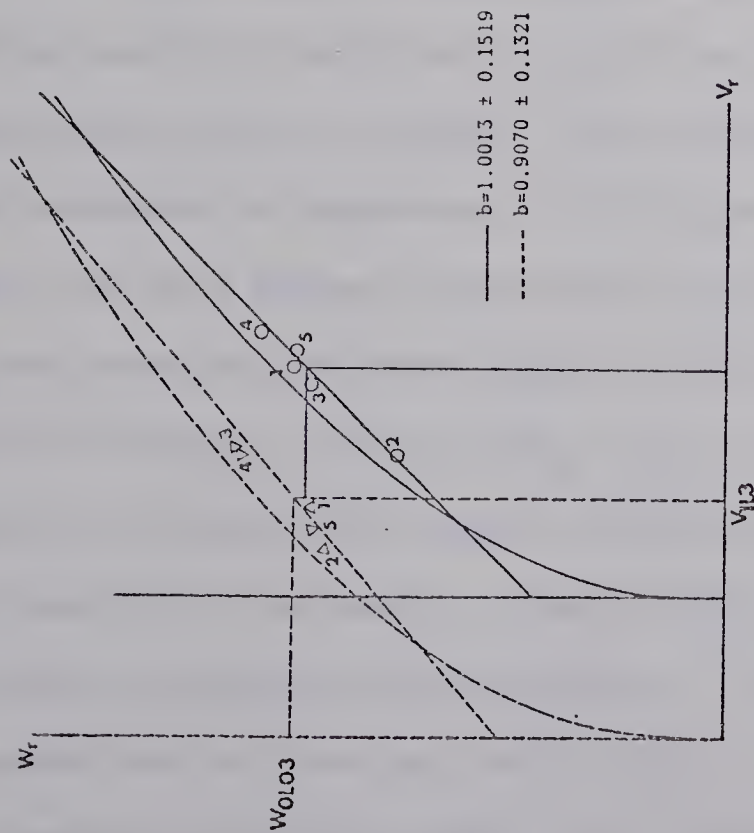


Figure 67. W_r, V_r graph for plant height from selfed backcross diallel set.

— $o = W_r, V_r$ intercepts at Ellerslie

--- $\Delta = W_r, V_r$ intercepts at Parkland

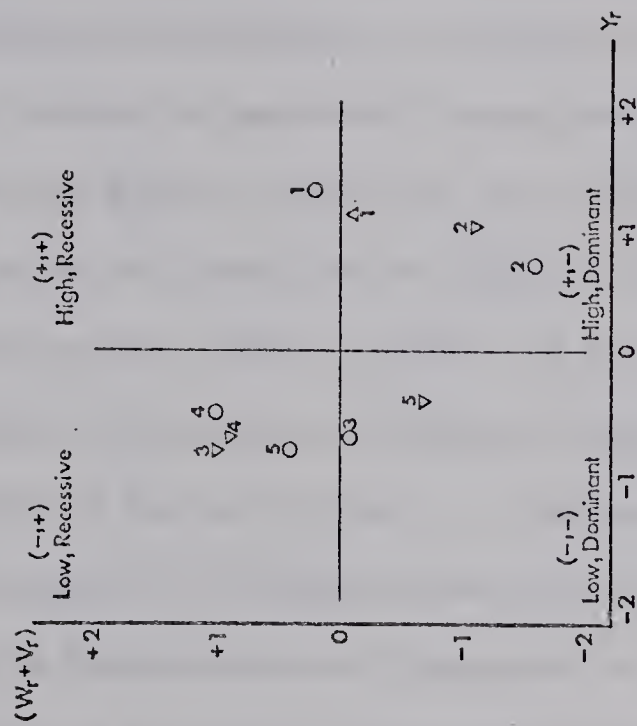


Figure 68. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for plant height from selfed backcross diallel set.

$o = Y_r, [W_r + V_r]$ intercepts at Ellerslie

$\Delta = Y_r, [W_r + V_r]$ intercepts at Parkland

locations, contributes to tallness, while the most recessives (Ciano and Khush-hal) contribute to shortness; i.e. the order of dominance of the parents is negatively correlated with their measurements. However, as shown in Table 79, the respective coefficients of correlation do not reach the 5% level of significance. The order of dominance of parents seems to differ at the two locations (Figure 68). The most recessive parent at Parkland (Khush-hal; -, + quadrant) possesses an excess of dominant genes (-, - quadrant) at Ellerslie, while Inia with an excess of recessive genes at Ellerslie (-, + quadrant), appears to have a preponderance of dominants at Parkland (-, - quadrant). Marquis, recessive at Ellerslie becomes dominant at Parkland. The ranking order of Ciano and Chinook remained unchanged. The coefficient of heritability was very high (91%) at both locations.

For number of tillers per plant, only the D and E components of variation were significant at Ellerslie, while all components except h^2 were significant at Parkland. Consequently, the proportional values of the estimates of parameters for Ellerslie data are not discussed. However, the mean degree of dominance may be given, since $(H_1 \div D)^{1/2} < 1$ for both locations indicating that tillering capacity is inherited as partially dominant. The ratio $[H_2 \div 4H_1] = 0.169$ at Parkland suggests asymmetry of positive and negative alleles at loci exhibiting dominance. The proportion of dominant to recessive genes in the parents is 2.58 indicating a preponderance of dominants. Since $[h^2/H_2] = 0.54$, it may be assumed that at least one group of genes exhibit dominance and control the inheritance of tiller number. The correlation coefficient between

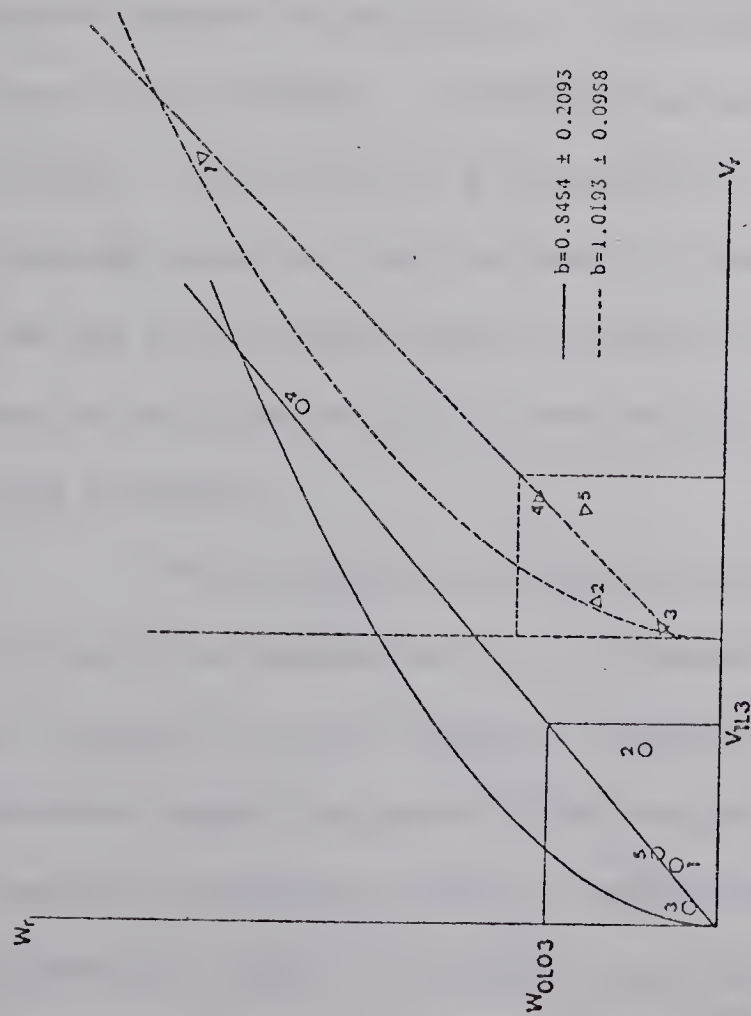


Figure 69. W_p , V_p graph for number of tillers per plant from selfed backcross diallel set.

— $o = W_p$, V_p intercepts
at Ellerslie
--- $\Delta = W_p$, V_p intercepts
at Parkland

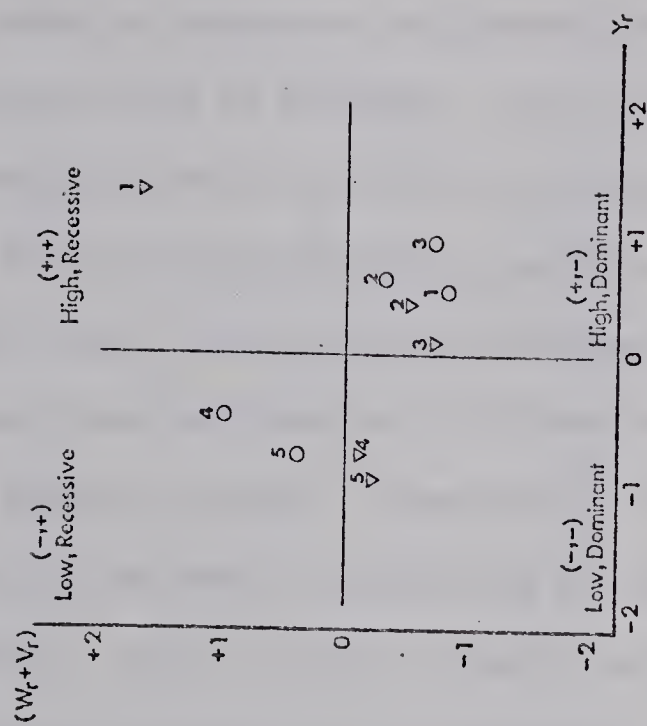


Figure 70. Standardized deviation graph of $[Y_p]$ and $[W_p + V_p]$ for number of tillers per plant from selfed backcross diallel set.

$o = Y_p$, $[W_p + V_p]$ intercepts
at Ellerslie
 $\Delta = Y_p$, $[W_p + V_p]$ intercepts
at Parkland

parental order of dominance and parental measurements is -0.748 at Ellerslie and 0.624 at Parkland. The significant negative correlation at Ellerslie indicates that the high tillering capacity is dominant over low tillering capacity while positive correlation at Parkland concludes that lower tiller number is dominant over higher. Figure 69 classifies Ciano and Khush-hal at Ellerslie as the most recessive and the most dominant parents, respectively. At Parkland, Marquis and Khush-hal are the most recessive and the most dominant parents, respectively. Figure 70 shows changes in the dominance ranking order of the parents between the two locations. Marquis, the most recessive parent at Parkland, (+,+ quadrant) appears to contain an excess of dominant genes at Ellerslie (+,- quadrant) while Ciano and Inia, recessive parents at Ellerslie (-,+ quadrant) appear as dominant at Parkland (-,- quadrant). Ranking order of Khush-hal and Chinook remain unchanged. The heritability estimates of 17.35% at Ellerslie and 72.28% at Parkland show that the character is highly unstable. This instability may be due to non-significance of genetic components of variation at Ellerslie and significance of environmental components of variation at both locations.

The results of diallel cross analysis from Tables 78 and 79 for number of spikelets per spike (Figures 71, 72), number of seeds per spike (Figures 73, 74), weight of seeds per spike (Figures 75, 76) and 1000-kernel weight (Figures 77, 78) may be interpreted in the same way as number of tillers per plant. Respective changes in the ranking order of parents for order of dominance and significance or non-significance

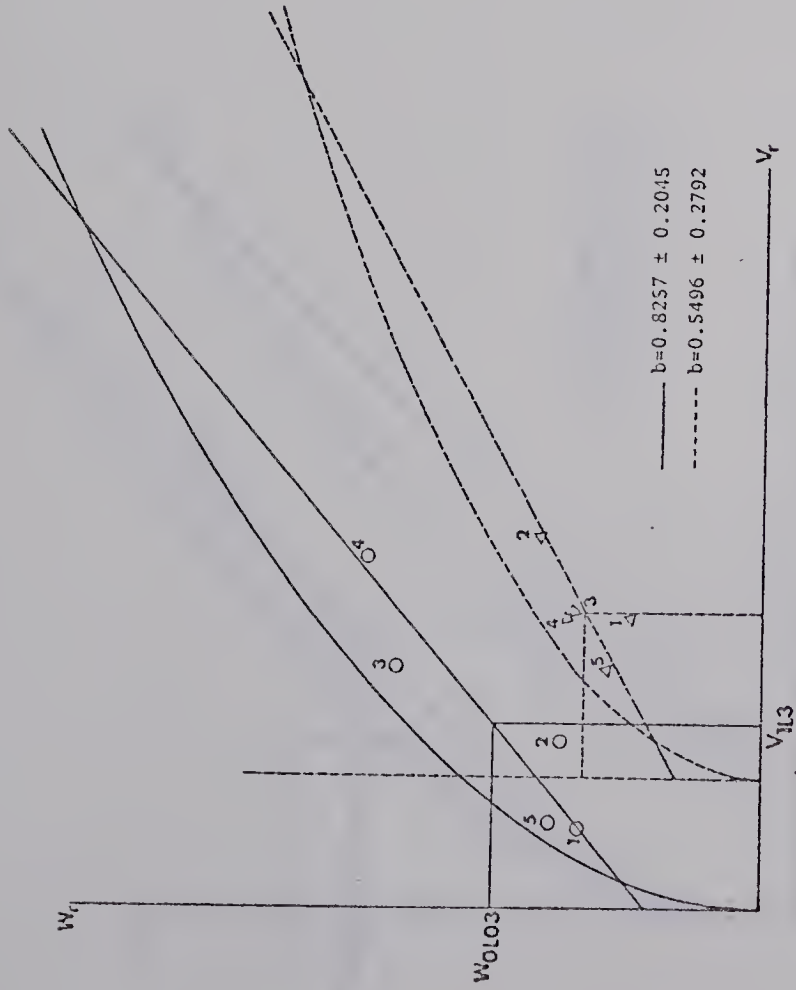


Figure 71. W_r, V_r graph for number of spikelets per spike from selfed backcross diallel set.

— $O = W_r, V_r$ intercepts at Ellerslie
--- $\Delta = W_r, V_r$ intercepts at Parkland

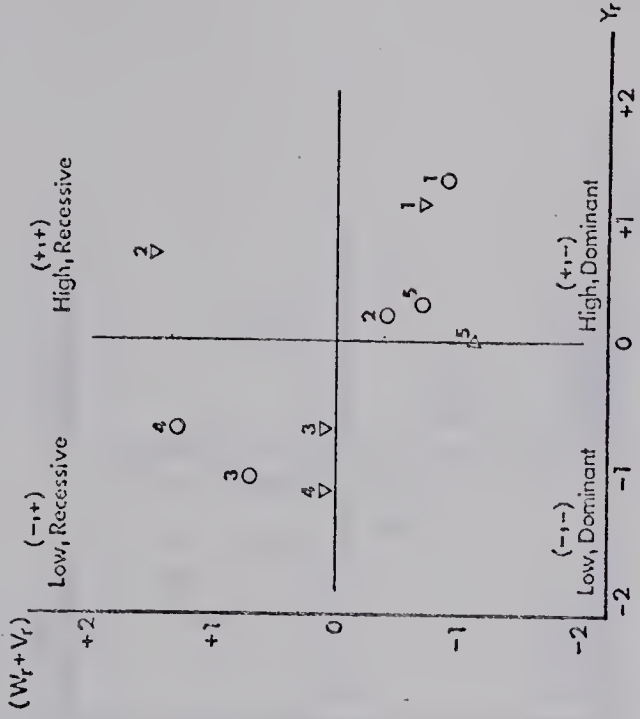


Figure 72. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of spikelets per spike from selfed backcross diallel set.

$O = Y_r, [W_r + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r, [W_r + V_r]$ intercepts at Parkland

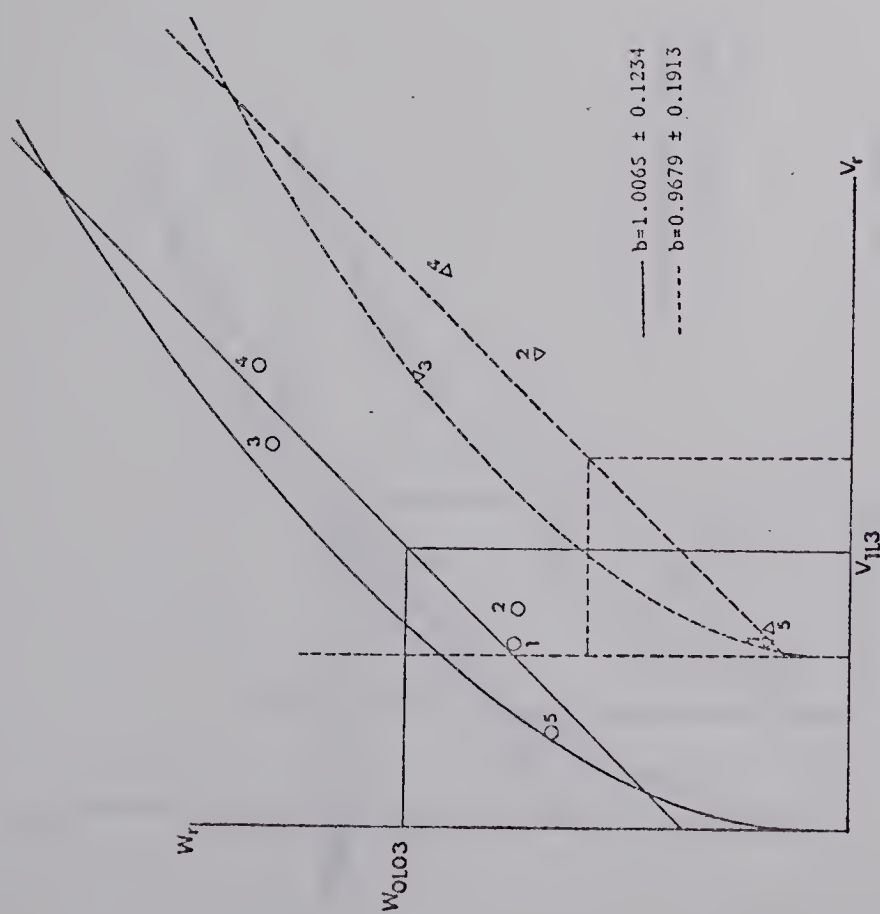


Figure 73. W_r , V_r graph for number of seeds per spike from selfed backcross diallel set.

— $o = W_r$, V_r intercepts
at Ellerslie
--- $\Delta = W_r$, V_r intercepts
at Parkland

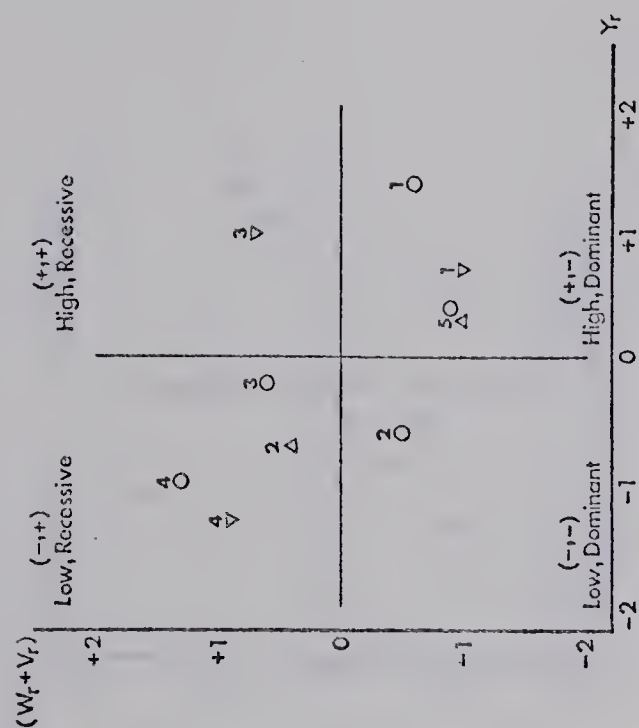


Figure 74. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of seeds per spike from selfed backcross diallel set.

$o = Y_r$, $[W_r + V_r]$ intercepts
at Ellerslie
 $\Delta = Y_r$, $[W_r + V_r]$ intercepts
at Parkland

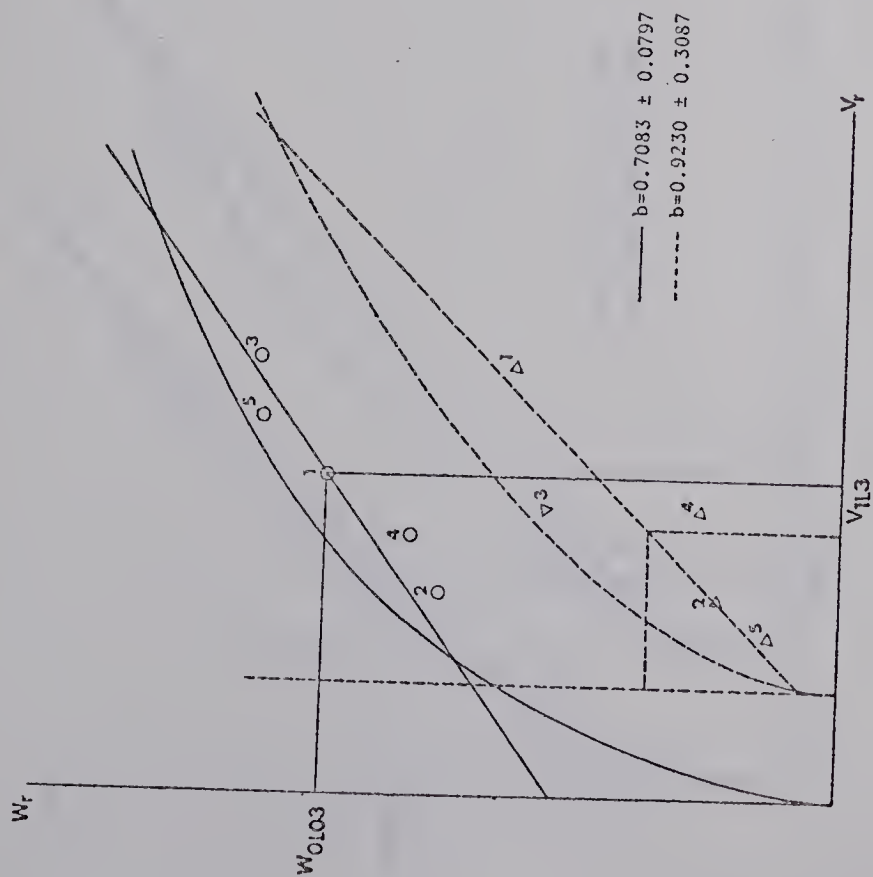


Figure 75. W_r , V_r graph for weight of seeds per spike from selfed backcross diallel set.

— $o = W_r, V_r$ intercepts at Ellerslie
--- $\Delta = W_r, V_r$ intercepts at Parkland

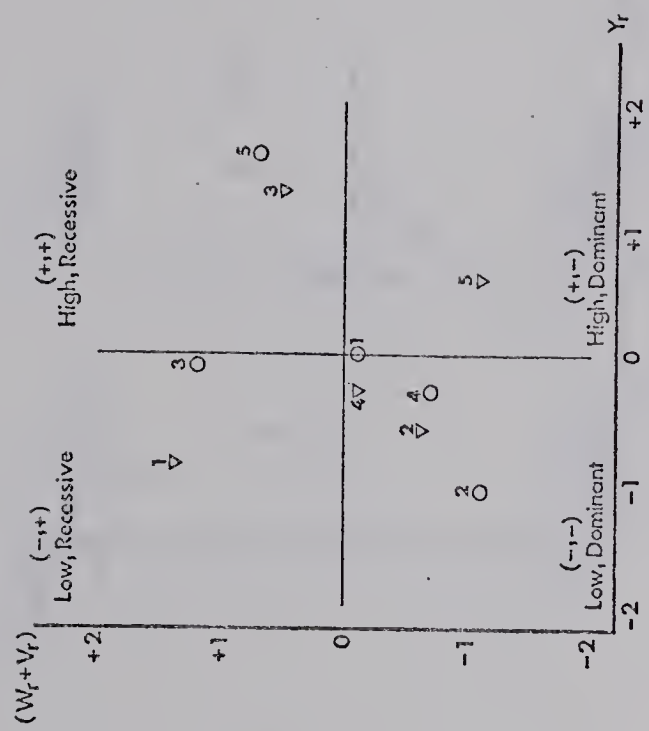


Figure 76. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for weight of seeds per spike from selfed backcross diallel set.

$o = Y_r, [W_r + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r, [W_r + V_r]$ intercepts at Parkland

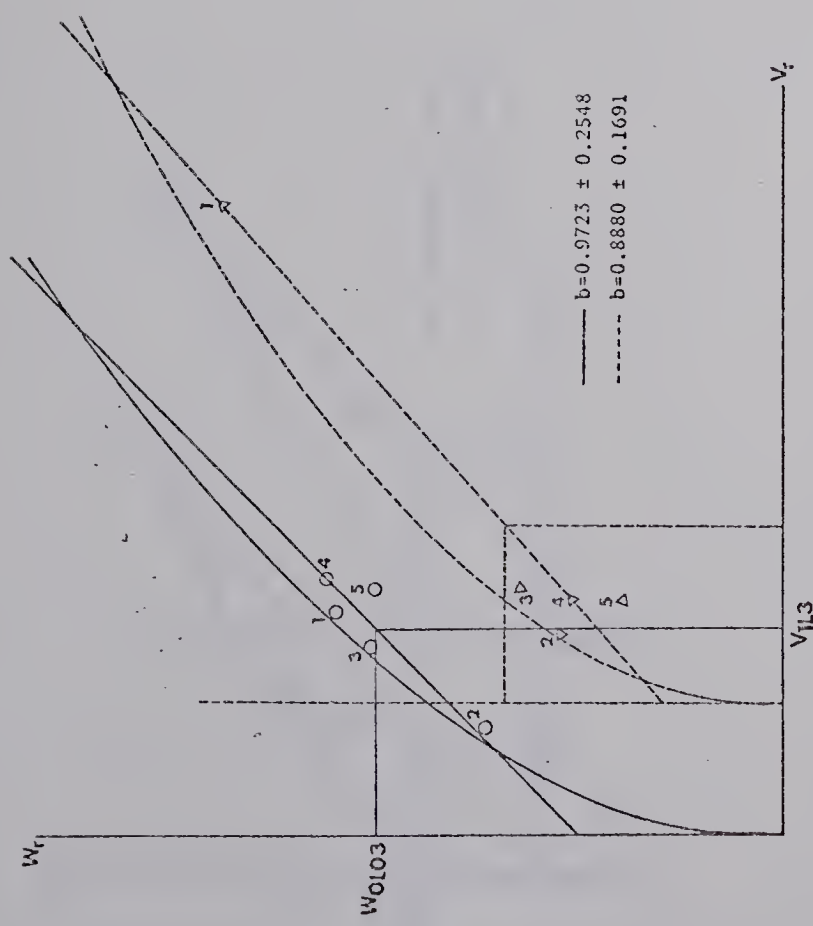


Figure 77. W_r, V_r graph for 1000-kernel weight from selfed backcross diallel set.

— $o = W_r, V_r$ intercepts at Ellerslie
--- $\Delta = W_r, V_r$ intercepts at Parkland

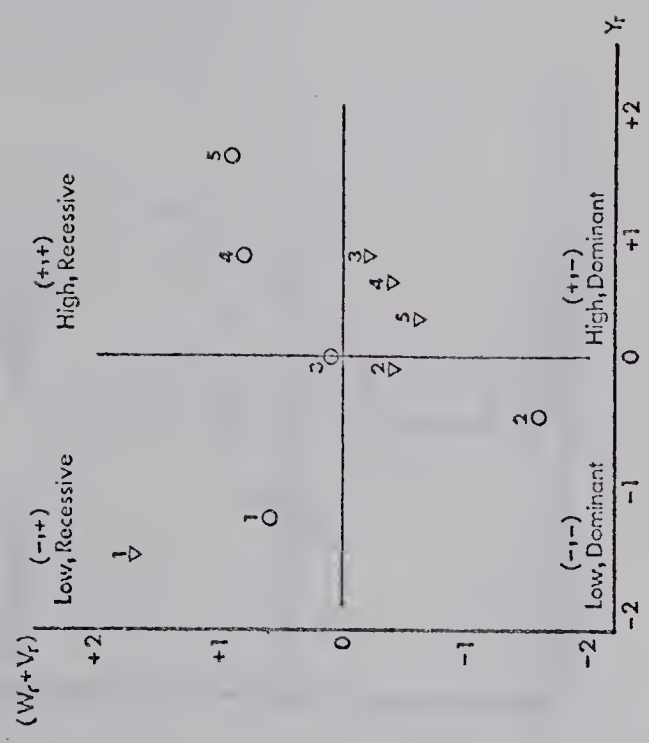


Figure 78. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for 1000-kernel weight from selfed backcross diallel set.

$o = Y_r, [W_r + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r, [W_r + V_r]$ intercepts at Parkland

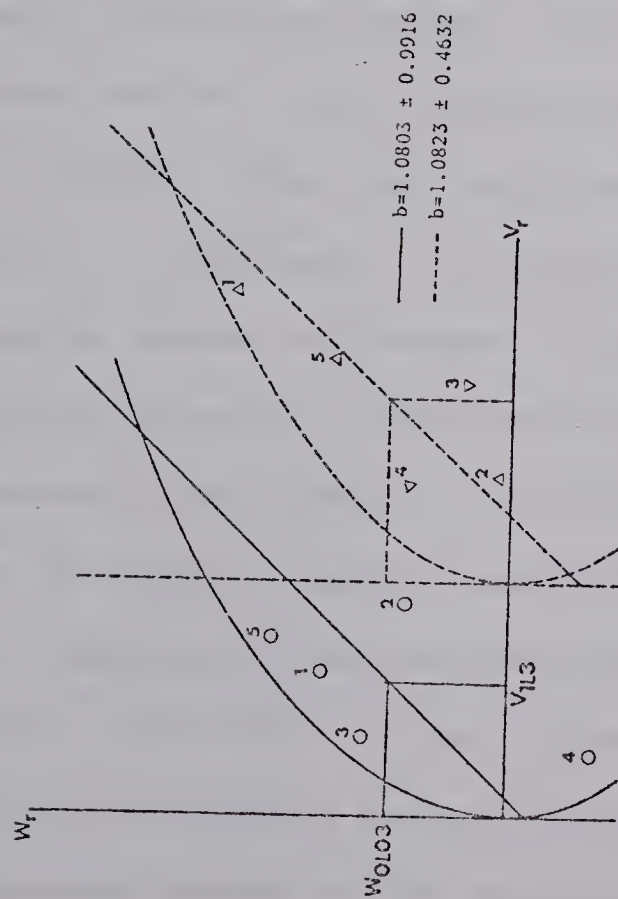


Figure 79. W_p, V_p graph for yield per plant from selfed backcross diallel set.

— $o = W_p, V_p$ intercepts at Ellerslie

--- $\Delta = W_p, V_p$ intercepts at Parkland

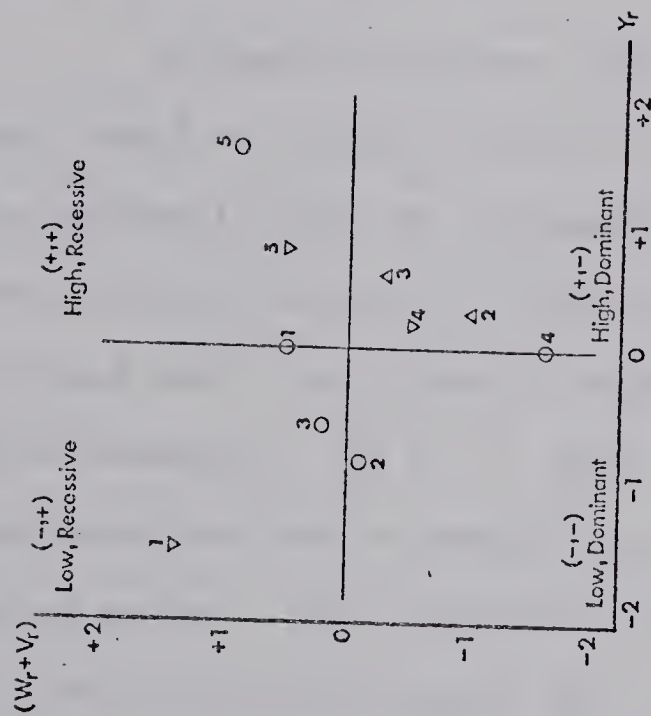


Figure 80. Standardized deviation graph of $[Y_p]$

and $[W_p + V_p]$ for yield per plant from selfed backcross diallel set.

$o = Y_p, [W_p + V_p]$ intercepts at Ellerslie

$\Delta = Y_p, [W_p + V_p]$ intercepts at Parkland

of genetic components of variation over the two locations may be interpreted accordingly.

In case of yield per plant, all the components of variation except D and E at Ellerslie and E at Parkland were non-significant. The proportional values of the genetic parameters given in Table 79 therefore do not carry valid conclusions. The ratio $[H_1 \div D]^{1/2} > 1$ at Parkland and ≈ 1 at Ellerslie suggests over-dominance and nearly complete dominance. The W_r, V_r graph (Figure 79) shows over-dominance at both locations (the regression line intersects the limiting parabola below the origin). The correlation coefficient of 0.327 at Ellerslie and -0.594 at Parkland suggests that low yielding capacity is dominant over high yield at Ellerslie and vice versa at Parkland. Figure 79 categorizes Inia and Ciano as the most recessive and dominant parents, respectively, at Ellerslie, while Marquis and Chinook as the most recessive and dominant parents, respectively, at Parkland. Figure 80 suggests that the highly recessive parent at Ellerslie is high yielding (+,+ quadrant), while the highly recessive parent at Parkland is low yielding (-,+ quadrant). Figure 80 also reveals changes in the ranking of parents with respect to their order of dominance at both locations. Khush-hal, recessive low-yielding at Ellerslie, appears to be dominant high-yielding at Parkland. Marquis, the most recessive parent at Parkland, appears comparatively less recessive at Ellerslie. Inia, Chinook and Ciano remained unchanged. Heritability of 51% at Ellerslie and -0.0005 $\approx$ 0% at Parkland suggests, respectively, high and non-heritable nature of yield. This reflects the inter-location environmental effect on the inheritance of yield.

GENOTYPE-ENVIRONMENT INTERACTION

This section of the experimental results deals with the comparison of the estimates of factor loadings, general combining abilities and genetic components of variation obtained from the analyses of four diallel sets considered over two locations.

In order to assess the stability of five principal factors with respect to their loadings on different characters, the varimax rotated factor matrices of F_1 , F_2 , backcross and selfed backcross diallel sets were factorially analysed for two locations. The results of analysis of variance are given in Table 80. Significance of mean squares for principal factors (F) and Characters (C) (upper part of Table 80) suggests that the number of factors required to explain the variability in the data varies with the number and the degree of expression of the characters under study. This is also indicated by significant $F \times C$ interaction, which implies that the differences between the contributions of different characters to factor loadings vary with the number of principal components. Significant inter-location effects (L) indicate differences in scores on the characters related to different principal components at different locations. Significance of the second order interaction, $L \times F \times C$, may be considered as interactions of the $L \times F$ with C, $L \times C$ with F, or of $F \times C$ with L. Since $L \times C$ is not significant, indicating that characters do not vary with locations, the $L \times F \times C$ interaction may be interpreted in the light of $L \times F$ and $F \times C$ interactions alone. In the first case, $L \times F \times C$ indicates that after pooling the sum of squares

TABLE 80

Factorial analysis of variance of factor loadings
of varimax rotated factor matrices of F1, F2, backcross
and selfed backcross diallel sets over two locations.

Source of variation	D.F.	Sum of squares	Mean squares	F ratio
Locations (L)	1	0.23868	0.23868	5.15589*
Principal factors (F)	4	2.73528	0.68382	14.77165**
L x F	4	2.39790	0.59947	12.94968**
Generations (G)	3	0.07528	0.02509	0.54210
L x G	3	0.08975	0.02991	0.64629
F x G	12	0.54642	0.04503	0.97284
L x F x G	12	0.19273	0.01606	0.34695
Characters (C)	9	1.80613	0.20068	4.33507**
L x C	9	0.76141	0.08460	1.82754
F x C	36	22.47183	0.62421	13.48413**
G x C	27	0.54033	0.02001	0.43230
L x F x C	36	7.44184	0.20671	4.46545**
L x G x C	27	0.91759	0.03398	0.73413
F x G x C	108	12.82314	0.11837	2.56482**
Error (L x F x G x C)	108	4.99961	0.04629	-
Locations	1	0.23868	0.23868	1.76766
Principal factors	4	2.73528	0.68382	5.06437**
L x P	4	2.39790	0.59974	4.43972**
Error	390	52.66000	0.13502	-

* Significant at 5% level

**Significant at 1% level

for characters into error sum of squares, the values of factor loadings vary at each location, and in the second case, it shows that the score of factor loadings on each character varies with the number of principal factors, considered independently of locations. Similarly, significant $F \times G \times C$ interaction may be interpreted considering the interactions of $F \times G$ with C , $F \times C$ with G and $G \times C$ with F . Since $F \times G$ and $G \times C$ are non-significant, the significance of $F \times G \times C$ in the presence of a significant $F \times C$ means that different factor loadings are carried by characters when averaged over generations.

Generations do not seem to have any effect on the factor loadings nor do they show interaction with principal factors, locations and characters. When the sum of squares for generations are pooled into error (lower part of Table 80), the location effects are not significant but the principal components are, with significant $L \times F$ interactions. It follows, therefore, that though on the average there is no significant location effect, the $L \times F$ interaction is significant. Thus the contributions of different factor loadings on different characters at different locations are not the same.

The factorial analysis of variance on weighted values for general combining abilities over four generations and two locations is given in Table 81. Individual GCA's were standardized by dividing each value of a particular character by the GCA, averaged over four generations and two locations, for that character. The aim of such standardization preceding *factorial ANOVA* was to normalize the scales for different characters. For example, heading data were taken in number of days,

TABLE 81

Factorial analysis of variance of general combining ability
over four generations and two locations.

Source of variation	D.F.	Sum of squares	Mean squares	F ratio
Locations (L)	1	1.71959	1.71959	1.15079
Parents (P)	4	2.54764	0.63691	0.42623
L x P	4	1.11852	0.27963	0.18713
Generations (G)	3	4.27284	1.42428	0.95316
L x G	3	1.78580	0.59526	0.39837
P x G	12	6.27137	0.52261	0.34975
L x P x G	12	3.89558	0.32463	0.21725
Error	360	537.93774	1.49427	-
Locations (L)	1	1.71959	1.71959	1.88320
Parents (P)	4	2.54764	0.63691	0.69752
L x P	4	1.11852	0.27963	0.30624
Generations (G)	3	4.27284	1.42428	1.55981
L x G	3	1.78580	0.59526	0.65191
P x G	12	6.27137	0.52261	0.57234
L x P x G	12	3.89558	0.32463	0.35552
Characters (C)	9	12.89835	1.43315	1.56952
L x C	9	8.39985	0.93331	1.02213
P x C	36	91.33239	2.53701	2.77842***
G x C	27	21.10522	0.78167	0.85606
L x P x C	36	192.26447	5.34067	5.84888***
L x G x C	27	21.24818	0.78696	0.86185
P x G x C	108	92.07365	0.85253	0.93366
Error (L x P x G x C)	108	98.61607	0.91311	-

***Significant at 0.1% level

plant height was measured in centimeters, yield per plant, weight of seeds per spike and 1000-kernel weight were expressed in grams, and number of tillers per plant, number of spikelets per spike and number of seeds per spike were scored as counts. Thus by dividing the GCA of each character by its mean over two locations, the scale differences were removed but the inter-location differences were preserved.

The first part of Table 81 shows a three-way layout analysis of general combining abilities where locations, parents and generations have been treated as main effects. None of the mean squares showed significance. This means that parental lines did not differ in their general combining abilities over the two locations in any generation of the diallel cross. When the characters were introduced as a fourth main effect by analyzing the normalized GCA's in a four-way factorial layout (second part of Table 81), the mean squares for $P \times C$ and $L \times P \times C$ interaction were significant. This suggests that the combining ability values for different characters vary with the number of parents and locations.

It is interesting to note that after introducing characters as separate effects, the mean squares, either for generations or any of the interactions involving generations, were not significant. This indicates that generations do not affect GCA's for any characters in question. The significance of $P \times C$ and $L \times P \times C$ interactions on the other hand provides the possibility for comparing which of the parental lines for their relative adaptability is more

TABLE 82

Analysis of variance of Parkland GCAs' regression
upon Ellerslie GCAs' regression for each of the parental lines

Parent	Source of variation	D.F.	Sum of squares	Mean squares	Regression coefficient
Marquis	Due to regression	1	157.5731	157.5731***	b = 0.9416
	Due to error	8	1.8675	0.2334	
Chinook	Due to regression	1	138.6222	138.6222***	b = 1.1118
	Due to error	8	1.3375	0.1671	
Khush-hal	Due to regression	1	62.7426	62.7426***	b = 1.0769
	Due to error	8	4.2024	0.5253	
Ciano	Due to regression	1	60.1872	60.1872***	b = 1.1163
	Due to error	8	1.0378	0.1297	
Inia	Due to regression	1	75.7396	75.7396***	b = 0.8821
	Due to error	8	0.4692	0.0586	

***Significant at 0.1% level

adaptive. For this purpose the GCA's for all the characters (averaged over all generations) at Parkland were regressed for each of the parental lines upon those at Ellerslie. The regression coefficients and the sums of squares due to regression and error partitioned for each cultivar are given in Table 82. It may be pointed out that unweighted GCA's (original values) were used in regression analysis since the effect of change in the degree of expression of one character relative to the other can be studied regardless of the unit of scale used. Significance of mean squares due to regression (Table 82) indicates that for every unit of change in GCA's at Ellerslie there is a corresponding proportional change for the corresponding GCA's at Parkland.

The genetic components of variation (from unadjusted treatment means) D , F and H_1 were considered themselves as variables and factorially analysed over generations and locations in order to study their consistency over the two environments. Before performing the *factorial ANOVA*, the values of genetic components for each character were standardized at each location. Thus, each D value was divided by the V_{OLO} for the same character, generation and location. Similarly, F 's were divided by their corresponding mean covariances (W_{OL01} in F_1 diallel, W_{OL02} in F_2 and backcross diallels and W_{OL03} in the selfed backcross diallel) and H_1 's by their respective mean variances (V_{1L1} in F_1 diallel, V_{1L2} in F_2 and backcross diallels and V_{1L3} in the selfed backcross diallel). Thus, for example, the F for number of tillers per

TABLE 83

Factorial analysis of variance of genetic components of variation over generations and locations. The sum of squares are respectively partitioned for D , H_1 and F .

Component	Source of variation	D.F.	Sum of squares	Mean squares	F ratio
D	Locations	1	0.14331	0.14331	1.10820
	Generations	3	0.03167	0.01055	0.08164
	Location x Generation	3	0.07301	0.02433	0.18820
	Error	72	9.31106	0.12932	
H_1	Locations	1	10.38381	10.38381	7.77135***
	Generations	3	2.16681	0.72227	0.54056
	Location x Generation	3	1.10066	0.36688	0.27458
	Error	72	96.20391	1.33616	
F	Locations	1	15.78510	15.78150	7.34709***
	Generations	3	7.28304	2.42768	1.13021
	Location x Generation	3	0.43955	0.14651	0.06821
	Error	72	154.65565	2.14799	

***Significant at 0.1% level

plant at Ellerslie in the selfed backcross diallel set of Table 78 was divided by the corresponding V_{OL03} from Table 77 (at Ellerslie) as follows: $-0.4873 \div 0.6890 = -0.7072$.

The process of standardizing the scale is analogous to Allard's technique, where prior to *factorial ANOVA*, each variance and covariance was divided by V_{OL0} of the respective block for that character (Allard 1956; Crumpacker and Allard 1962). In the present study additive $[D]$, dominance $[H_1]$ and additive x dominance $[F]$ components are subsequently considered separately and analysed independently for their stability over generations and locations. The reciprocals of the variances of the parents of the array mean variances and of the array mean covariances were used as weights in standardizing the values of D 's, H_1 's and F 's respectively. The use of these different multipliers in normalizing the scale effects preserved the order of magnitude of respective parameters. The *factorial ANOVA* on the weighted values of D 's, H 's and F 's is given in Table 83. The results show that additive effects of the genes (component D) are the same for two locations. Dominance gene effects (component H_1) and additive x dominance effects (component F) differ significantly at the two locations. On the whole, generations do not seem to affect the values of genetic components of variation. Significant mean squares for locations with respect to H_1 and F raise the question of the heterogeneity of location effects on the parameters in different generations. To answer this, the unweighted values of D 's, H_1 's and F 's at Parkland were respectively regressed for each generation upon those of Ellerslie, and

TABLE 84

Analysis of variance of regression of genetic components of variation
of Parkland upon those of Ellerslie for each generation.

Component	Generation	Source of variation	D.F.	Mean squares	F value
Additive Component [D]	F ₁ diallel	Due to regression	1	228657.5229	4578.6540***
		Due to error	8	49.9399	r = 0.9990 b = 1.0658
	F ₂ diallel	Due to regression	1	227792.7663	3549.9323***
		Due to error	8	64.1682	r = 0.9998 b = 1.0603
Dominance Component [H ₁]	Backcross diallel	Due to regression	1	228207.7135	4597.8009***
		Due to error	8	49.6341	r = 0.9990 b = 1.0630
	Selfed back- cross diallel	Due to regression	1	229349.4236	4251.7073***
		Due to error	8	53.9429	r = 0.9990 b = 1.0642
	F ₁ diallel	Due to regression	1	1532.9815	81.7304***
		Due to error	8	18.7562	r = 0.9534 b = 0.8233
	F ₂ diallel	Due to regression	1	2001.8299	391.1351***
		Due to error	8	5.1180	r = 0.9898 b = 1.3637
Additive x dominance Component [F]	Backcross diallel	Due to regression	1	2619.8806	74.1992***
		Due to error	8	35.3087	r = 0.9500 b = 2.4385
	Selfed back- cross diallel	Due to regression	1	412.1566	39.0566***
		Due to error	8	10.5528	r = 0.9109 b = 1.0823
	F ₁ diallel	Due to regression	1	812.9743	80.8326***
		Due to error	8	10.0575	r = 0.9538 b = 0.4664
	F ₂ diallel	Due to regression	1	1190.1414	31.2178***
		Due to error	8	38.1237	r = -0.8921 b = -1.4409
Backcross diallel	Backcross diallel	Due to regression	1	40.3149	2.8143
		Due to error	8	14.3248	r = 0.5100 b = 0.3220
Selfed back- cross	Selfed back- cross	Due to regression	1	8.6977	0.8605
		Due to error	8	10.1077	r = 0.3098 b = 0.3603

***Significant at 0.01% level

the sum of squares of deviations were partitioned into variation due to regression and remainder (error). Extremely high variance ratios (Table 84) for the parameters D and H_1 , and close agreements between the coefficients of correlation and regression, both in sign and magnitude, indicate stability of these parameters over the two locations. The case of parameter F is rather confusing. The diallels based on backcross and selfed backcross generations show a lack of correspondence between F values at the two locations (variance ratio for regression non-significant). This may be ascribed to a change of relationship between additive and dominance gene effects ($F = \Sigma dh$) caused by altered environmental conditions. A more drastic relational change is that between the F_1 and F_2 generations of the diallel sets ($r = 0.95$, $b = 0.47$ and $r = -0.89$, $b = -1.44$, respectively). It is rather difficult to think of a logical explanation for this reversed relationship.

Since, on the whole, generation did not significantly affect the genetic components of variation, their estimates were obtained by solving, least-square-wise, the following system of linear equations, where the known terms, i.e., the array variances and covariances for a given generation were obtained by using adjusted treatment means from analysis of variance as a partially balanced lattice design:

$$\text{(Parents):} \quad D + E - V_{0L0} = d_1$$

$$F_1 \text{ diallel:} \quad (1/2)D - (1/4)F + (1/5)E - W_{0L01} = d_2$$

TABLE 85

Components of genetic variation obtained from statistics based on adjusted treatment means
for ten characters over four generations at two locations.

Character	D	F	H ₁	H ₂	E
Onset-of-heading	6.3534 ± 0.7633** 8.8228 ± 2.7613**	9.2901 ± 1.7240** 11.7467 ± 6.2367	13.8477 ± 3.1070** 24.7571 ± 11.2393	10.6407 ± 2.7703** 21.4808 ± 10.0215	1.2748 ± 0.7546 2.7428 ± 2.7299
Final heading	9.9906 ± 1.4371** 7.8483 ± 3.7575	15.6860 ± 3.2459** 10.9821 ± 8.4667	18.0874 ± 5.8495** 20.9983 ± 15.2940	12.6612 ± 5.2157* 18.3467 ± 13.6368	3.6999 ± 1.4207 3.6404 ± 3.7147
Heading-span	0.3776 ± 0.1378* 0.5506 ± 0.0782**	0.8367 ± 0.3114* 1.7013 ± 0.1767**	1.2987 ± 0.5612 4.6086 ± 0.3185**	0.9496 ± 0.5004 3.4230 ± 0.2640**	0.6144 ± 0.1363** 0.4756 ± 0.0773**
Plant height	40.1899 ± 194.6123 15.6247 ± 324.5877	-139.3000 ± 439.5492 -384.9300 ± 733.1102	-194.3550 ± 792.1188 -274.4790 ± 321.1500	-26.7551 ± 706.2876 88.9778 ± 177.9948	329.6460 ± 192.3959 324.0350 ± 320.8911
Number of tillers per plant	0.4516 ± 0.5333 1.4083 ± 0.1271**	1.3445 ± 1.2047 1.9880 ± 0.2871**	-1.0911 ± 2.1710 6.3148 ± 0.5175**	-1.5535 ± 1.9358 5.3106 ± 0.4614**	1.9733 ± 0.5273** 0.2227 ± 0.1257
Number of spikelets per spike	0.7624 ± 0.1544** 0.1911 ± 0.0835	1.1451 ± 0.3489* 0.2397 ± 0.1887	0.8665 ± 0.6287 1.3766 ± 0.3402**	0.5013 ± 0.5606 1.3117 ± 0.3033**	0.5284 ± 0.1527** 0.1653 ± 0.0826**
Number of seeds per spike	10.0189 ± 3.2757* 9.0891 ± 1.0313	15.8223 ± 7.3986 19.5596 ± 2.3293**	26.9036 ± 13.3331 48.6433 ± 4.1977	17.6712 ± 11.8884 30.0795 ± 3.7429**	13.0569 ± 3.2384** 0.2803 ± 1.0195
Weight of seeds per spike	0.0139 ± 0.0025** 0.0194 ± 0.0071**	0.0146 ± 0.0058** 0.0389 ± 0.0161**	-0.0113 ± 0.0105 0.0239 ± 0.0291	-0.0191 ± 0.0094** 0.0064 ± 0.0259	0.0209 ± 0.0025** 0.0170 ± 0.0070**
1000-kernel weight	5.0333 ± 1.2956** 9.2436 ± 3.0167*	7.6451 ± 2.9262** 16.2749 ± 6.8136*	11.5453 ± 5.2734 19.2289 ± 12.2789	7.9758 ± 4.7020 11.4570 ± 10.9484	3.9945 ± 1.2808* 2.6902 ± 2.9824
Yield per plant	1.8082 ± 0.7141* -1.1075 ± 0.1948**	3.4802 ± 1.6130 -1.9481 ± 0.4400**	4.9964 ± 2.9068 -4.3292 ± 0.7930**	3.3320 ± 2.5918 -3.4484 ± 0.7071**	2.5752 ± 0.7060** 2.3649 ± 0.1926**

The first reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level

** Significant at 1% level

$$\begin{aligned}
& (1/4)D - (1/4)F + (1/4)H_1 + (3/5)E - V_{1L1} = d_3 \\
& (1/4)D - (1/4)F + (1/4)H_1 - (1/4)H_2 + (1/10)E - V_{0L1} = d_4 \\
F_2 \text{ diallel: } & (1/2)D - (1/8)F + (1/5)E - W_{0L02} = d_5 \\
& (1/4)D - (1/8)F + (1/16)H_1 + (3/5)E - V_{1L2} = d_6 \\
& (1/4)D - (1/8)F + (1/16)H_1 - (1/16)H_2 \\
& + (1/10)E - V_{0L2} = d_7 \\
\text{Backcross} \\
\text{diallel: } & (1/2)D - (1/8)F + (1/5)E - W_{0L02} = d_8 \\
& (1/4)D - (1/8)F + (1/16)H_1 + (2/5)E - V_{1L2} = d_9 \\
& (1/4)D - (1/8)F + (1/16)H_1 - (1/16)H_2 \\
& + (7/100)E - V_{0L2} = d_{10} \\
\text{Selfed backcross} \\
\text{diallel: } & (1/2)D - (1/16)F + (1/5)E - W_{0L03} = d_{11} \\
& (1/4)D - (1/16)F + (1/32)H_1 + (2/5)E - V_{1L3} = d_{12} \\
& (1/4)D - (1/16)F + (1/32)H_1 - (1/32)H_2 \\
& + (7/100)E - V_{0L3} = d_{13}
\end{aligned}$$

In this system of equations $d_{K=1,2,\dots,13}$ denotes the difference between the expected and observed values of the k th statistic. The environmental component of variation (E) was accounted for by using the multiplier $(1/2)$ when F_1 and F_2 generations, and $(1/4)$ when backcross and selfed backcross generation diallel sets were considered (Hayman 1958). The solutions of this system of equations for the various components of variation are shown in Table 85. Error terms were calculated in a manner usual to the unweighted least square solution, i.e. as $\pm (\sum_k d_k c_{ii} \div DF)^{1/2}$, where c_{ii} is the appropriate term on the main diagonal of the variance-covariance matrix of the coefficients,

TABLE 86

Estimates of genetic parameters from diallel analysis
of adjusted treatment means for ten characters over four generations at two locations.

Character	$[H_1 \div D^{1/2}]$	$[H_2 \div 4H_1]$	$\left[\frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F} \right]$	Heritability
Onset-of-heading	1.4763* 1.6751	0.1921* 0.2169	2.9621* 2.3189	0.3968 0.2689
Final heading	1.3455* 1.6356	0.1750* 0.2184	3.8012* 2.4948	0.3674 0.2420
Heading-span	1.8545 2.8931*	0.1827 0.1856*	3.9680 3.2920*	0.1145 0.1027
Plant height	2.1990 4.1886	0.0344 -0.0810	0.1188 -0.4922	0.0308 0.0109
Number of tillers per plant	1.5543 2.1175*	0.3559 0.2102*	46.3456 1.9999*	0.0764 0.2125
Number of spikelets per spike	1.0660 2.6839	0.1446 0.2382*	5.7672 1.6100	0.2935 0.0960
Number of seeds per spike	1.7276 2.3135	0.1642 0.1545	2.8599 2.7392	0.1366 0.2312
Weight of seeds per spike	0.9016 1.1099	0.4225 0.0669	3.7901 23.2285	0.1941 0.2679
1000-kernel weight	1.5144 1.4422	0.1727 0.1489	3.0116 4.1330	0.2020 0.4026
Yield per plant	1.6622 1.9770*	0.1667 0.1991	3.7498 0.3842	0.1327 -0.1855

First reading under each column refers to Ellerslie and the second to Parkland

*The parameters involved are significantly different from zero (Table 85)

and D.F. = 13 - 5 = 8 (thirteen equations, five fitted parameters). For one set of paradoxical results (significant negative values of D , H_1 and H_2 for yield per plant at Parkland), the source of error could not be determined.

The proportional estimates of genetic parameters obtained from Table 85 are given in Table 86. The data indicate that all characters are inherited as over-dominant traits at both locations, except for weight of seeds per spike at Ellerslie which showed nearly complete dominance, i.e. $(H_1 \div D)^{1/2} \approx 1$. Moreover $[(1/4DH_1)^{1/2} + F] \div [(1/4DH_1)^{1/2} - F] > 1$ in all cases, except for plant height at both locations and yield per plant at Parkland, suggests strongly a preponderance of dominant genes in the parents. When valid, $(H_2 \div 4H_1)$ was found to be less than 0.25, indicating thus a certain degree of numerical asymmetry of alleles with positive and with negative effects at loci showing dominance. Heritability values in all cases were low, the maximum being 40.26% (1000-kernel weight at Parkland).

The results of Table 86 when compared with those of Tables 20, 39, 60 and 79 show the effect of the adjustment factor characteristic of incomplete block designs. In the latter Tables, where genetic parameters have been estimated from analyses of F_1 , F_2 , backcross and selfed backcross diallel sets of unadjusted treatment means (treated as randomized block design), the values of $(H_1 \div D)^{1/2}$, $(H_2 \div 4H_1)$ and $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ show a wide range of variation from partial dominance to overdominance, from a fully symmetrical distribution of alleles with positive and negative effects to strong

TABLE 87

Analysis of variance of regression of genetic components of variation
at Parkland upon those at Ellerslie averaged over generations for all characters.

Component of variation	Source of variation	D.F.	Sum of squares	Mean squares	Coefficients of correlation & regression
Additive component [D]	Due to regression	1	228499.9514	228499.9514**	b = 1.0633
	Due to error	8	432.9894	54.1236	r = 0.9990
Dominance component [H ₁]	Due to regression	1	1561.3878	1561.3878**	b = 1.3188
	Due to error	8	65.5032	8.1879	r = 0.9796
Additive x Dominance Component [F]	Due to regression	1	306.8222	306.8222**	b = 1.0430
	Due to error	8	100.9412	12.6176	r = 0.8674
Additive component [D]	Due to regression	1	197.6459	197.6459**	b = 0.3825
	Due to error	8	90.3328	11.2916	r = 0.7579
Dominance component [H ₁]	Due to regression	1	76528.1655	75528.1655**	b = 1.4230
	Due to error	8	345.5664	43.1958	r = 0.9997
Additive x Dominance Component [F]	Due to regression	1	137604.3889	137604.3889**	b = 2.6663
	Due to error	8	963.3961	120.4245	r = 0.9964

The first part of the table refers to unadjusted treatment means (treated in randomized block design) and the second part refers to adjusted treatment means from partially balanced lattice design.

**Significant at 1% level

asymmetry, and from equal to unequal proportions of dominant to recessive alleles in the parents. Table 86 on the other hand shows that these ratios, especially those for valid parameters (* in Table 85), are more stable over characters since over-dominance in inheritance, asymmetry of alleles at loci exhibiting dominance, and inequality in the proportions of dominant and recessive alleles are constant features of the concerned characters.

The regression analysis of genetic components of variation D , H_1 and F for Ellerslie and Parkland, obtained first from unadjusted treatment means (randomized block design) averaged over generations, and then from adjusted treatment means of Table 85, is given in Table 87. The purpose of this analysis was to see whether there is concordance between the values of parameters evaluated from the data at the two locations separately. The results given in Table 87 show a good agreement in this respect between locations. Parameters D and F evaluated from array variances and covariances from unadjusted treatment means show the same rates of change from character to character at the two locations ($b \approx 1$). For H_1 this change is $b = 1.32$ at Parkland for unit change at Ellerslie. With adjustment of treatment means the situation is changed, so that for unit change at Ellerslie there is a change of $b = 0.38$ for D and $b = 2.67$ for F at Parkland. The corresponding change for H_1 is less pronounced ($b = 1.32$) without adjustment as compared to $b = 1.42$ with adjustment.

The relationships between the two locations in regard to changes in D , H_1 and F for the various characters are shown graphically

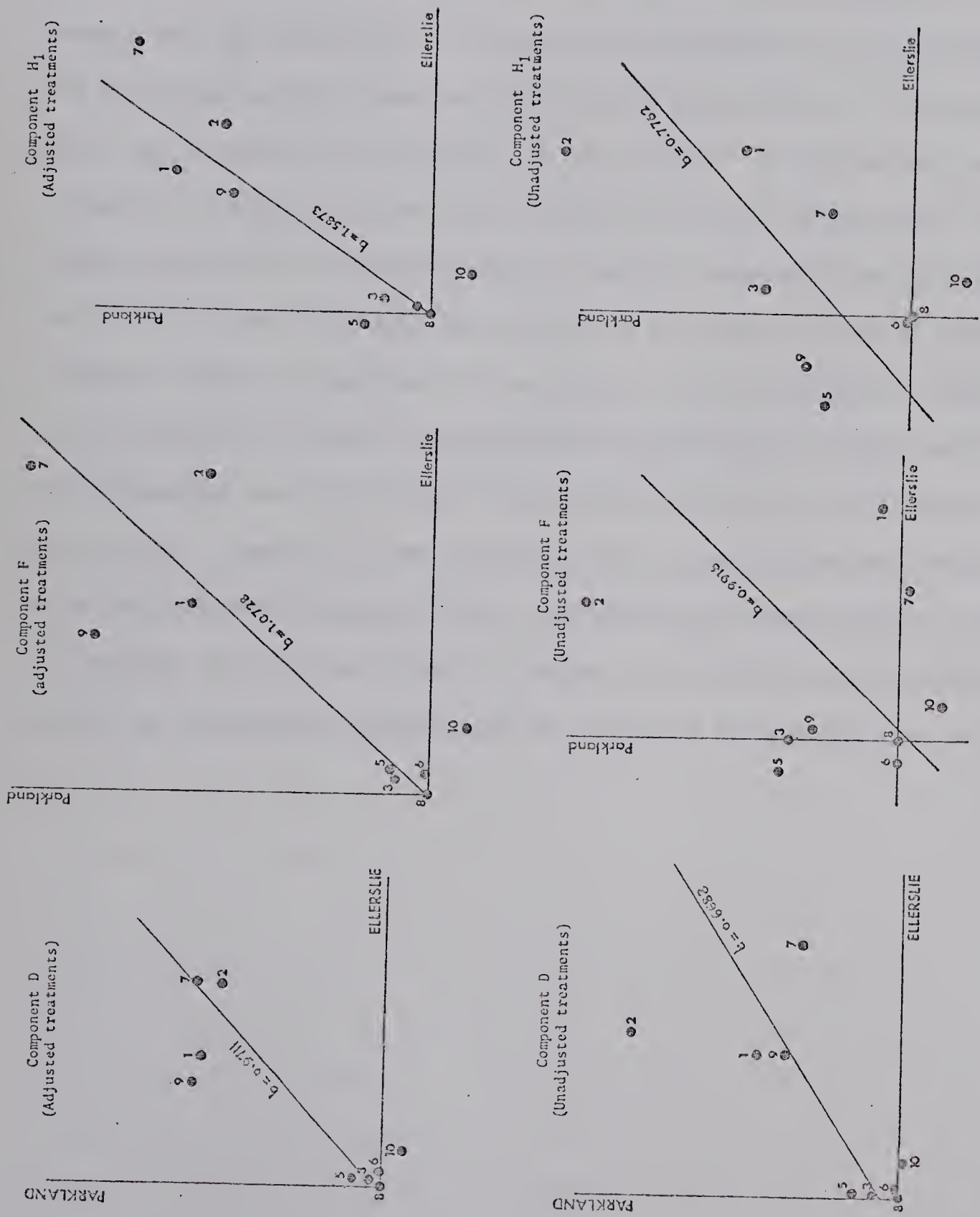


Figure 81. Regression of genetic components of variation at Parkland upon those at Ellerslie for all the characters except plant height. Solid circles refer to regression intercepts for different characters.

in Figure 81. The scatter of the intercept points around the regression lines shows that there are considerable discrepancies between the two locations. The points of intercepts for plant height are not shown in the graphs because of very high values of the components which far exceeded the boundaries of the graphs. Therefore the coefficients of regression were recalculated excluding plant height. It is rather difficult to determine either from the regression analysis of Table 87 or from the graphs whether and by how much the use of adjusted treatment means has improved the estimates of the parameters. Hence it is not possible to assess the parametric relationships within and between the characters and within and between the locations or environments. Nevertheless, looking at the graphs of the parameters derived beginning with the adjusted treatment means, one would be rather strongly inclined to conclude that the adjustment of means has considerably improved the degree of concordance between the two locations with respect to parameters.

DISCUSSION

The F_1 , F_2 , backcross and selfed backcross generations of five parent diallel cross of common wheat (*Triticum aestivum* L.) were grown in 1972 at two locations and the data obtained was analysed with respect to correlation between the characters, principal factors, general and specific combining abilities, genetic components of variation and environmental effects. The experimental design used was a partially balanced triple lattice. However, most of the analyses were carried out both as a complete randomized block design and as a lattice design. The results obtained are discussed in sequel.

Correlation and factor analyses. Among the characters considered in this study, yield of grain per plant is agronomically the most important. Therefore the knowledge of its correlation with other characters is of importance from a theoretical and a practical point of view. The results of the correlation analyses of F_1 , F_2 , backcross and selfed backcross diallel sets are given in Tables 2, 21, 42, and 61. These results show that early maturing entries have produced high yields and the late maturing ones low yields of grain per plant. As expected, there was a positive correlation between yield per plant and most of its subcharacters or components. A strong positive association was found to exist between the subcharacters, number of tillers per plant, weight of seeds per spike and 1000-kernel weight with yield per plant. The components, number of spikelets per spike and number of seeds per spike were not correlated with yield at either location in F_1 (Table 2) but were

positively correlated in the other generations of diallel cross either at both locations (Table 21) or at one of them (Tables 42 and 61). There was no correlation between yield and plant height.

The degree of expression of metrical characters (phenotypes) depends both on the genotypic constitution of the parents and the environmental conditions under which the experimental materials are grown. Therefore the comparison of results obtained by various researchers using different sets of parents and carried out under different environmental conditions lead only to non-related or loosely-related general information. For example, Lee and Kaltsikes (1973) working with durum wheat in Winnipeg have found that the characters days-to-maturity and yield per plant were positively correlated in both the F_1 and the F_2 generations of a 10 x 10 diallel cross, whereas in the present study of all the generations of diallel cross the correlation was negative. On the other hand, Hsu (1970) has found that in the F_1 generation of a five-parent diallel cross of common wheat there was no correlation between anthesis date (final heading) and yield per plant, a result similar to that found in the present case at Parkland. Although Hsu has conducted his study in Edmonton, the two experiments were spaced in time, and except for Inia, the parental lines used were different. The significant positive association of yield per plant with its components found in this study was also observed in the works of Johnson and Schmidt (1968), Smocek (1969), Lebsock and Amaya (1969), Hsu and Walton (1970), Kaltsikes and Lee (1971), Lee and Kaltsikes (1973) and Chebib *et al* (1973). The absence of correlation between plant height

and yield per plant in the present study was also observed by Kaltsikes and Lee (1971) and Chebib *et al* (1973). These results are in disagreement with those of some other experiments [Lebsock and Amaya (1969), Kaltsikes and Larter (1970) and Lee and Kaltsikes (1973)].

The relationship between individual characters is rather complicated. Therefore the data were subjected to factor analysis. This analysis provides information on contributions of independent variables relative to those of dependent ones. The results of the factor analysis of F_1 , F_2 , backcross and selfed backcross data obtained for two locations are shown in Tables 3, 22, 43 and 62, and the principal factors have been interpreted earlier. The first principal factor, *lateness*, has negative loading for yield per plant and the highest positive loading for onset-of-heading and final heading. This confirms the conclusion arrived at earlier, that the majority of late-heading entries have produced low grain yields per plant. The degree of expression of heading-span was found to be correlated with final heading but not with onset-of-heading. It was not correlated with yield in F_1 and F_2 but was positively associated with it in backcross and selfed backcross data. This inconsistency suggests that heading-span is not one of the characters affecting yield per plant. In fact the factor analyses based on the F_1 , F_2 backcross and selfed backcross diallel sets have revealed positive factor loadings for heading-span and negative ones for yield. It follows therefore that positive correlations of heading-span with yield per plant at Parkland in the backcross and selfed backcross diallel sets does not necessarily imply

a cause-and-effect relationship, and may in fact be attributed to strong environmental influence upon particular entries of the diallel table.

The second principal factor, termed differently in different generations, carried the highest loadings for number of spikelets per spike, number of seeds per spike and weight of seeds per spike except the backcross diallel at Parkland (Table 43), for which plant height had the highest loading. A similar situation was observed with respect to principal factors 3, 4 and 5 which had their highest loadings from different characters in different generations of the diallel cross. Thus it appears that different factors operate differently in different populations (generations) though they share the same gene pool.

Combining ability analyses. The results of the analyses of data for general and specific combining abilities with respect to the characters considered have shown that the parents with high GCA's do not necessarily produce hybrids with high SCA's. The comparisons of GCA's with SCA's for all the generations and characters are collected in Table 88. Of all the comparisons, eighty to be exact, 84% constitute cases in which high SCA's are associated with one or both parents having low GCA's, and *vice versa*. These observations are in agreement with those reported by Crumpacker and Urquhart (1962), Fonseca (1965), Brown *et al* (1966), Gyawalli *et al* (1968) and Singh *et al* (1969) in wheat. Analogous results have been observed by Larson (1941) in tomatoes, and

by Walker (1963), Chang (1967), Soomro (1967), Baluch and Soomro (1969) and Soomro and Baluch (1969) in cotton. On the other hand Kime (1950) and Hawkins *et al* (1965) working with cotton have found that GCA and SCA were positively correlated so that the present results are in contradiction to their reports.

Significant variances of general and specific combining abilities for a particular character denote, respectively, the importance of additive and non-additive gene effects for that character. If the variance for specific combining ability for a particular character is significant and that for general combining ability is not, selection for the character will be on the basis of SCA. On the other hand, high SCA variances associated with a particular parent, even if it has high GCA, reflect an inconsistency in the performance of that parent with respect to the particular character (Griffing, 1956) and indicate that the hybrids involved with that parent would perform poorer than would be expected on the basis of their specific combining abilities. It follows therefore that in combining ability screening tests a pedigree selection procedure would be expected to screen out the strains with considerably larger SCA variances.

In the present studies variances of general combining ability were generally larger than those of specific combining ability for all characters, and diallel-set generations at both locations (Tables 5 to 14, 24 to 33, 45 to 54 and 64 to 73). There were a few cases where the estimates of SCA variances were higher than those for GCA's, but the magnitudes of their differences were negligible. This

would indicate a high consistency of performance of the parental lines an observation which may also be generally verified by their general combining ability values (Tables 4, 23, 44 and 63), and more specifically from the results of Table 82. The significance of variances for general and specific combining abilities were examined from Tables 15, 34, 55 and 74. In general, the mean squares for GCA were significant for all characters except heading-span and yield per plant at one or both the locations. Such significances of GCA mean squares are not uncommon in wheat (Brown *et al* 1966, Fonseca 1965, Paroda and Joshi 1970a, Parodi *et al* 1970 and Bitzer *et al* 1971). Mean squares for SCA were significant only for a few characters.

It may be pointed out that a high general combining ability for some characters as for example onset-of-heading and final heading may not be desirable under certain circumstances. High GCA for these characters implies lateness, so that when selecting for earliness, lines with the lowest GCA's must therefore be given priority. In the present study Ciano and Inia had the lowest GCA's for heading data, and consequently selection from their progenies is expected to result in early lines. Plant height is another character for which the selection of wheat cultivars with low GCA's may be desirable.

Diallel cross analysis. The analysis of variance of diallel tables according to Hayman (1954a) gave *a* component significances (for additive gene effects) in all generations of the diallel cross (Tables 16, 35, 56 and 75) for all the characters except heading-span and yield per plant

(Tables 16 and 35) and yield per plant (Tables 56 and 75). These results corresponded to those for general combining ability in *ANOVA*'s (Tables 15, 34, 55 and 74). Thus Hayman's α component and Griffing's GCA are analogous. Genetic components of variation for each generation of the diallel cross have shown values ranging from non-significance to high significance. The only paradoxical ones are the negative but significant D 's and H_1 's of Tables 19, 38, 59 and 78, which may be ascribed to high environmental variation. Such unexpected values are not uncommon (Mather 1949, Wright 1952, Newell 1970 and Holmes 1972) in biometrical genetics. The interpretation of genetic parameters in such cases becomes questionable.

Proportional values of the estimates of genetic parameters viz., $(H_1 \div D)^{1/2}$, $(H_2 \div 4H_1)$, $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ and $[h^2/H_2]$ for characters studied in different generations of the diallel cross ranged from partial dominance to over-dominance, from complete symmetry to strong asymmetry in distribution of genes with positive and negative effects in the parents, from equal proportions of dominant and recessive genes in the parents to a preponderance of dominants or recessives, and from high to low numbers of gene groups controlling a particular character. Heritability estimates also showed a wide range of values, from -0.1129 (yield per plant, Table 39) to +1.085 (onset-of-heading, Table 79), indicating in this example, a complete lack of heritability for yield and an extremely high heritability for earliness. Quite low heritability estimates of yield in wheat have been reported by a number of researchers (Wiebel 1956, McNeal 1960,

Kronstad and Foot 1964, Johnson *et al* 1966, and Paroda and Joshi 1970, 1970a).

Genotype-environment interaction. The assessment of genetic and environmental components of variation with respect to a character depends upon the gene pool involved and the non-hereditary factors constituting the environment in which the experimental material is grown. The choice of statistical approach varies with the type of data available and the object of the study. In this study *factorial ANOVA* and regression analysis (Mather, 1951) were used to assess the degree of discordance between identical sets of materials grown at two locations with respect to factor loadings for the various characters, general combining abilities of the parents and the main genetic components of variation.

The factor loadings on various characters seemed to be different for the two locations (Table 80). The effect of generations on factor-loading scores for different characters was negligibly small. In fact none of the interactions involving generation were significant. This finding contradicts that of Lee and Kaltsikes (1973) who found discrepancies between their F_1 and F_2 diallel factor analyses with respect to the factor loading scores on various characters. They attributed these generation differences to a considerable difference in plot size for the two generations, and difference in planting techniques viz., space-planting for F_1 diallel and solid planting for F_2 diallel. In the present case, though plot size, planting techniques and experimental

set up was the same, nevertheless, the environmental conditions at the two locations were quite different. In spite of significant inter-location effects, different generations proved to be fairly homogeneous with regard to factor loadings.

In the *factorial ANOVA* for general combining abilities of the four generations of the diallel cross and the two locations (Table 81) it was found that the GCA values were more or less the same. However, when characters were treated separately in the analysis (*ANOVA* assumed single observation per cell), GCA's differed between locations. These results indicate that parents did not differ in GCA's over the two locations when their GCA's were averaged over all characters, but they certainly did when considered individually for each character. The response of each variety with respect to additive gene effects was studied after averaging the GCA's of a cultivar over four generations of the diallel cross and regressing the estimates obtained at one location upon those of the other. In the analysis of variance for regression (Table 82) the inter-location effects were found to be homogeneous for each variety. In other words, the GCA's for the two locations were concordant. The variances for general and specific combining ability also did not differ significantly at the two locations. Moreover, the conspicuous feature of the combining ability analysis was the high consistency with which the GCA variances were higher than the corresponding SCA variances at both locations. This in fact shows the stability of cultivars over locations according to Griffing's (1956) enunciation.

The stability of genetic components of variation, viz., D , H_1 and F was assessed over the two locations through *factorial ANOVA*. The results indicated (Table 83) that there was no significant difference between locations for any component. Moreover, the generations, on the whole, did not affect these parameters at either location. But when the estimates of one component for Parkland were regressed upon those of Ellerslie it was found that the selfed back-cross generation of the diallel cross was affecting the component F . This constituted a significant change in the relationship between additive and dominance gene effects in the progeny of the backcrosses. Moreover the estimates of the F component for the two locations were correlated differently in the F_1 and F_2 generations ($+r$ and $-r$ respectively). It is rather difficult to think of a logical explanation for this change of relationship between additive and dominance gene effects [$\Sigma(d) \times \Sigma(h)$] in two generations of the same diallel set.

The occurrence of significant negative values for genetic components of variation was an unexpected feature of diallel cross analysis for which a satisfactory interpretation is lacking. Such values have been reported in a number of instances (Mather 1949, Wright 1952, Newell 1970 and Holmes 1972) but a logical explanation for their occurrence has not been given. The frequency of their occurrence appear to be too high to be attributed to chance.

BIBLIOGRAPHY

- AALDERS, L.E. and D.L. CRAIG (1968). General and specific combining ability in seven inbred strawberry lines. *Can. Jour. Genet. Cytol.*, 10: 1-6.
- AKSEL, R. and L.P.V. JOHNSON (1961). Genetic studies on sowing-to-heading and heading-to-ripening periods in barley and their relation to yield and yield components. *Can. Jour. Genet. Cytol.*, 3: 242-259.
- AKSEL, R. and L.P.V. JOHNSON (1963). Analysis of a diallel cross: A worked example. *Advancing Frontiers of Plant Science (India)*, 2: 37-53.
- ALLARD, R.W. (1956). The analysis of genotype-environmental interactions by means of diallel crosses. *Genetics*, 41: 305-318.
- ALLARD, R.W. (1961). Relationship between genetic diversity and consistency of performance in different environments. *Crop Sci.*, 1: 127-133.
- ALLARD, R.W. and P.L. WORKMAN (1963). Population studies in predominantly self pollinated species. IV. Seasonal fluctuations in estimated values of genetic parameters in lima bean populations. *Evolution*, 17: 470-480.
- ANAND, I.J. and B.R. MURTY (1968). Performance of heterozygotes in presence of reciprocal and maternal effects in diallel crosses of linseed. *Ind. Jour. Genet. Plant Breed.*, 28:
- ANAND, I.J. and B.R. MURTY (1969). Serial analysis of combining ability in diallel and fractional diallel crosses in linseed. *Theoret. Appl. Genetics*, 39: 88-94.
- ATHWAL, D.S. and G. SINGH (1966a). Variability in Kangni. I. Adaption, genotypic and phenotypic variability in four environments. *Ind. Jour. Genet. Plant Breed.*, 26: 142-152
- ATHWAL, D.S. and G. SINGH (1966b). Variability in Kangni. II. Genotype x environment interaction, heritability and genetic advance. *Ind. Jour. Genet. Plant Breed.*, 26: 153-161.
- BAGNARA, D. (1967). A diallel analysis of quantitative characters in varieties and radio induced mutant lines of *Triticum durum*. *Genetica Agraria*, 21: 313-337.

- BAKER, R.J. (1969). Genotype-environment interactions in yield of wheat. *Can. Jour. Plant Sci.*, 49: 743-751.
- BALUCH, M.A. and B.A. SOOMRO (1969). Combining ability for seed and lint-index in *Gossypium arboreum* L. *Pakistan Cottons*, 13: 116-128.
- BAUMAN, L.F. (1959). Evidence of non-allelic gene interaction in determining yield, ear height and kernel row number in corn. *Agron Jour.*, 51: 531-534.
- BHATT, G.M. (1971). Heterotic performance and combining ability in a diallel cross among spring wheats (*Triticum aestivum* L.). *Aust. Jour. Agric. Res.*, 22: 359-368.
- BITZER, M.J., F.L. PATTERSON and W.E. NYQUIST (1971). Hybrid vigour and gene action in a six parent diallel cross of soft winter wheat. *Can. Jour. Genet. Cytol.*, 13: 131-137.
- BREESE, E.L. (1969). The measurement and significance of genotype-environment interactions in grasses. *Heredity*, 21: 387-397.
- BROWN, C.M., R.O. WIEBEL and R.D. SEIF (1966). Heterosis and combining ability in common winter wheat. *Crop Sci.*, 6: 382-383.
- BUCIO ALANIS, L. (1966). Environmental and genotype-environmental components of variability. I. Inbred lines. *Heredity*, 21: 387-397.
- BUCIO ALANIS, L. (1966a). Environmental and genotype-environmental components of variability. II. Heterozygotes. *Heredity*, 21: 399-405.
- CARNAHAN, H.L. (1947). Combining ability in flax. M.S. Thesis, University of Minnesota, St. Paul, Minn., U.S.A.
- CATTEL, R.B. (1965). Factor Analysis: An introduction to essentials. I. The purpose and underlying models. *Biometrics*, 21: 190-215.
- CHANG, M.A. (1967). Combining ability in *Gossypium hirsutum* L. Unpublished M.Sc. (Agriculture) Thesis, University of Sind, Hyderabad, Pakistan.
- CHEBIB, F.S., S.B. HELGASON and P.J. KALTSIKES (1973). Effect of variation in plant spacing, seed size and genotype on plant-to-plant variability in wheat. *Z. Pflanzenzuchtg*, 69: 301-332.

- CHENG, C.L. and T.Z. CHANG (1970). Diallel analysis of agronomic traits in rice (*Oryza sativa* L.). Bot. Bull. of Academia Sinica, (New Series), 11: 61-78.
- CHIANG, M.S. (1969). Diallel analysis of the inheritance of quantitative characters in cabbage (*Brassica oleracea* L. *Var. capitata* L.). Can. Jour. Genet. Cytol., 11: 103-109.
- CHIANG, M.S. and J.D. SMITH (1967a). Diallel analysis of inheritance of quantitative characters in grain sorghum. I. Heterosis and inbreeding depression. Can. Jour. Genet. Cytol., 9: 44-51.
- CHIANG, M.S. and J.D. SMITH (1967b). Diallel analysis of inheritance of quantitative characters in grain sorghum. II. Gene action, the number of effective factors and heritability. Can. Jour. Genet. Cytol., 9: 823-830.
- COCHRAN, W.G. and G.M. COX (1957). Experimental designs. Second edition. John Wiley and Sons, Inc., New York. xiv+611 pp.
- CRUMPACKER, D.W. and R.W. ALLARD (1962). A diallel cross analysis of heading date in wheat. Hilgardia, 32: 275-318.
- CRUMPACKER, D.W. and N.S. URQUHART (1962). Relationship of gene action and combining ability in set of wheat parents. Abstr., Annual meeting, Amer. Soci. Agron., Cornell Univ., Ithaca, page 65.
- DUNN, G.M. and J.A. WRIGHT (1970). Performance of diallel crosses of *Bromus inermis* for forage yield. Crop Sci., 10: 56-58.
- DURRANT, A. (1965). Analysis of reciprocal differences in diallel crosses. Heredity, 20: 573-607.
- DURRANT, A. and H. TYSON (1964). A diallel cross of genotypes and genotrophs of *Linum*. Heredity, 19: 207-227.
- EAGLES, C.F. (1967). The effect of temperature on vegetative growth in climatic races of *Dactylis glomerata* in controlled environments. Ann. Bot., 31: 31-39.
- EBERHART, S.A. and W.A. RUSSELL (1966). Stability parameters for comparing varieties. Crop Sci., 6: 36-40.
- EBERHART, S.A. and W.A. RUSSELL (1969). Yield and stability for a 10-line diallel of a single-cross and double-cross maize hybrids. Crop Sci., 9: 357-361.

- EUNIS, A.M., L.P.V. JOHNSON and R. AKSEL (1962). Inheritance of winter hardiness in an eighteen parent diallel cross of barley. *Can. Jour. Genet. Cytol.*, 4: 356-376.
- FASOULAS, A.C. and R.W. ALLARD (1962). Non-allelic gene interactions in the inheritance of quantitative characters in barley. *Genetics*, 47: 899-907.
- FINLAY, K.W. and G.N. WILKINSON (1963). The analysis of adaptation in the plant breeding programme. *Austr. Jour. Agric. Res.*, 14: 742-754.
- FONSECA, S.M. (1965). Heterosis, heterobeltiosis, diallel analysis and gene action in crosses of *Triticum aestivum*. Unpublished Ph.D. Thesis, Purdue University, U.S.A. *Diss. Abstr.*, 26: 4153.
- FONSECA, S.M. and F.L. PATTERSON (1968). Hybrid vigour in a seven parent diallel cross in common winter wheat (*Triticum aestivum* L.). *Crop Sci.*, 8: 85-88.
- FRYXELL, P.A., G. STATEN and J.H. PORTER (1958). Performance of some wide crosses in *Gossypium*. *New Mex. Agric. Expt. Sta. Bult.*, 419: 1-15.
- GRIFFING, B. (1956). Concept of general and specific combining ability in relation to diallel crossing systems. *Austr. Jour. Biol. Sci.*, 9: 463-493.
- GRISSOM, D.B. and R.R. KALTON (1956). Inheritance of combining ability for forage traits in brome grass (*Bromus inermis* Leyss.). *Agron. Jour.*, 48: 289-293.
- GYAWALI, K.K., C.O. QUALSET and W.T. YAMAZAKI (1968). Estimates of heterosis and combining ability in winter wheat. *Crop. Sci.*, 8: 322-324.
- HARMAN, H.H. (1960). Modern factor analysis. Second edition. The University of Chicago Press, Chicago, U.S.A.
- HAWKINS, B.S., H.A. PEACOCK and W.W. BALLARD (1965). Heterosis and combining ability in upland cotton. Effect on yield. *Crop Sci.*, 5: 543-546.
- HAYMAN, B.I. (1954a). Analysis of variance of diallel tables. *Biometrics*, 10: 235-244.
- HAYMAN, B.I. (1954b). Theory and analysis of diallel crosses. I. *Genetics*, 39: 789-809.
- HAYMAN, B.I. (1958). Theory and analysis of diallel crosses. II. *Genetics*, 43: 63-85.
- HAYMAN, B.I. (1960). Theory and analysis of diallel crosses. III. *Genetics*, 45: 155-172.

- HILL, J. and J.M. PERKINS (1969). The environmental induction of heritable changes in *Nicotiana rustica*. Effects of genotype-environment interactions. *Genetics*, 61: 661 - 675.
- HOLMES, T.M. (1972). A quantitative genetic analysis of avoidance behaviour in *Mus musculus*. M.Sc. Thesis, The University of Alberta, Edmonton, Canada.
- HOTELLING, H. (1933). Analysis of a complex of statistical variables into principal components. *Jour. Edu. Psychol.*, 24: 417-441 and 498-520.
- HSU, PING-HWA (1970). Inter-relationships and inheritance of agronomic and morphological characters in spring wheat. M.Sc. Thesis, The University of Alberta, Edmonton, Canada.
- HSU, P. and P.W. WALTON (1970). The inheritance of morphological and agronomical characters in spring wheat. *Euphytica*, 19: 54-60.
- HULL, F.H. (1945). Regression analysis of yield of hybrid corn and inbred parental lines. *Maize Genet. Newsletter*, 19: 21-27.
- JINKS, J.L. (1954). Analysis of continuous variation in a diallel cross of *Nicotiana rustica* varieties. *Genetics*, 39: 767-788.
- JINKS, J.L. (1956). The F_2 and backcross generations from a set of diallel crosses. *Heredity*, 10: 1-30.
- JINKS, J.L. and B.I. HAYMAN (1953). The analysis of diallel crosses. *Maize Genet. Newsletter*, 27: 48-54.
- JINKS, J.L., J.M. PERKINS and S.R. GREGORY (1972). The analysis and interpretation of differences between reciprocal crosses of *Nicotiana rustica* varieties. *Heredity*, 28: 363-377.
- JOHNSON, L.P.V. and R. AKSEL (1959). Inheritance of yielding capacity in a fifteen parent diallel cross of barley. *Can. Jour. Genet. Cytol.*, 1: 208-265.
- JOHNSON, L.P.V. and R. AKSEL (1964). The inheritance of malting quality and agronomic characters in a diallel cross of barley. *Can. Jour. Genet. Cytol.*, 6: 178-200.
- JOHNSON, V.A. and J.W. SCHMIDT (1968). Hybrid wheat. *Adv. Agron.*, 20: 199-233.
- JOHNSON, V.A., K.B. BIEVER, A. HAUNOLD and J.W. SCHMIDT (1966). Inheritance of plant height, yield of grain and other plant and seed characteristics in a cross of hard red winter wheat, *Triticum aestivum* L. *Crop Sci.*, 6: 336-338.

- JOHNSTON, T.D. (1968a). A biometrical approach to plant breeding. 5th. Congress of the European Assoc. for research on plant breeding, Milano, Italy, page 97-107.
- JOHNSTON, T.D. (1968b). Studies on a diallel cross and double-cross hybrids among various *Brassica oleracea* types. *Euphytica*, 17: 63-73.
- KALTSIKES, P.J. (1970). Genotype-environment interaction variances in yield trials of fall rye. *Can. Jour. Plant Sci.*, 50: 77-80.
- KALTSIKES, P.J. and N.E. LARTER (1970). The interaction of genotype and environment in *durum* wheat. *Euphytica*, 19: 236-242.
- KALTSIKES, P.J. and J. LEE (1971). Quantitative inheritance in *durum* wheat. *Can. Jour. Genet. Cytol.*, 13: 210-218.
- KEHR, W.R. (1961). General and specific combining ability for four agronomic traits in a diallel series among six alfalfa clones. *Crop Sci.*, 1: 53-55.
- KEMPTHORNE, O. (1956). The theory of diallel cross. *Genetics*, 41: 451-459.
- KIHARA, H. (1944). Die Entdeckung der DD-analysatoren bei weizen. *Agric. Hort. (Tokyo)*, 19: 839-890.
- KIHARA, H. and F.A. LILIENFELD (1949). A new synthesized 6x-wheat. *Proc., Intern. Congress of Genetics*, 8th., 307-319.
- KIME, P.H. (1950). Hybrid vigour in upland cotton. Effect on yield and yield quality. *Proc., Sec. Cotton Imp. Conf., Biloxi, Miss., U.S.A. (Mimeograph)*.
- KINMAN, M.L. and G.F. SPRAGUE (1945). Relation between number of parental lines and theoretical performance of synthetic varieties of corn. *Jour. Amer. Soci. Agron.*, 37: 341-351.
- KNIGHT, R. (1965). The relation between the yield and the reproductive phase in cocksfoot (*Dactylis glomerata* L.) in a winter rain-fall environment. *Austr. Jour. Agric. Res.*, 16: 505-515.
- KNIGHT, R. (1970). The measurement and interpretation of genotype-environment interactions. *Euphytica*, 19: 225-235.
- KNOWLES, R.P. (1950). Studies in combining ability in bromegrass and crested wheat grass. *Sci. Agric.*, 30: 275-302.
- KRONSTAD, W.E. and W.H. FOOTE (1964). General and specific combining ability estimates in winter wheat (*Triticum aestivum* L.). *Crop. Sci.*, 4: 616-619.

- LARSON, R.E. (1941). The F₁ combining ability of certain tomato varieties. Proc., Amer. Soci. Hort. Sci., 39: 313-314.
- LAWLEY, D.N. and A.E. MAXWELL (1963). Factor analysis as a statistical method. Butterworth, London. pp: 117.
- LEBSOCK, K.C. and A. AMAYA (1969). Variation and covariation of agronomic traits in *durum* wheat. Crop Sci., 9: 312-315.
- LEE, J. and P.J. KALTSIKES (1973). Multivariate statistical analysis of grain yield and agronomic characters in *durum* wheat. Theoret. Applied Genet., 43: 226-231.
- LEGG, P.D., G.B. COLLINS and C.C. LITTON (1970). Heterosis and combining ability in diallel crosses of burley tobacco, *Nicotiana tabacum* L. Crop Sci., 10: 705-707.
- LIANG, G.H. (1967). Diallel analysis of agronomic characters in grain sorghum, *Sorghum vulgare* Pers. Can. Jour. Genet. Cytol., 9: 269-276.
- LINAG, G.H. and T.L. WALTER (1966). Genotype x environment interactions from yield tests and their applications to sorghum breeding programs. Can. Jour. Genet. Cytol., 8: 306-311.
- LIANG, G.H., E.G. HEYNE, J.H. CHUNG and Y.O. KOH (1968). The analysis of heritable variation for three agronomic traits in a six-variety diallel of sorghum, *Sorghum vulgare* Pers. Can. Jour. Genet. Cytol., 10: 460-469.
- LUPTON, F.G.H. (1961). Studies in the breeding of self pollinated cereals. III. Further studies in cross prediction. Euphytica, 10: 209-224.
- LUPTON, F.G.H. (1965). Studies in the breeding of self pollinated cereals. V. Use of incomplete diallel in wheat breeding. Euphytica, 14: 331-352.
- MARANI, A. (1963). Heterosis and combining ability for yield and components of yield in diallel crosses of two species of cotton. Crop Sci., 3: 252.
- MARANI, A. and Y. SACHS (1966). Heterosis and combining ability in a diallel cross among nine varieties of oriental tobacco. Crop Sci., 6: 19-22.
- MATHER, K. (1949). Biometrical genetics. Methuen and Co., London.
- MATHER, K. (1951). Statistical analysis in biology. Fourth edition, Methuen and Co., London.

- MATHER, K. and J.L. JINKS (1971). Biometrical genetics. Second edition. Chapman and Hall Ltd., London. pp. 382.
- MATZINGER, D.F., G.F. SPRAGUE and C.C. COCKERHAM (1959). Diallel cross of maize in experiments repeated over locations and years. Agron. Jour., 51: 346-350.
- MATZINGER, D.F., J.J. MANN and C.C. COCKERHAM (1962). Diallel crosses in *Nicotiana tabacum*. Crop. Sci., 2: 383-386.
- McFADDEN, E.S. and E.R. SEARS (1944). The artificial synthesis of *T. spelta*. Rec. Genetics Soc. Amer., 13: 26-27.
- McFADDEN, E.S. and E.R. SEARS (1946). The origin of *Triticum spelta* and its free-threshing hexaploid relatives. Jour. Hered., 37: 81-89 and 107-116.
- McNEAL, F.H. (1960). Yield component in a Lemhi x Thatcher wheat cross. Agron. Jour., 52: 348-349.
- MELBURNE, M.C. and W.P. THOMPSON (1927). The cytology of a tetraploid wheat hybrid *Triticum spelta* x *Triticum monococcum*. Amer. Jour. Botany, 14: 327-333.
- MILLER, P.A. and A. MARANI (1963). Heterosis and combining ability in diallel crosses of upland cotton, *Gossypium hirsutum* L. Crop Sci., 3: 441-444.
- MOHAMMAD, A.H. and A.S. HANNA (1965). Inheritance of quantitative characters in rice. Can. Jour. Genet. Cytol., 7: 406-417.
- MORROW, E.B., R.E. COMSTOCK and T. KELLEHER (1958). Genetic variances in strawberries. Proc., Amer. Soci. Hort. Sci., 72: 170-185.
- MURTY, B.R., V. ARUNACHALAM and I.J. ANAND (1967). Diallel and partial diallel analysis of some yield factors in *Linum usitatissimum*. Heredity, 22: 35-41.
- NAKAMURA, N. (1956). Statistical studies on combining ability in maize. Hyago Noka Naigaku, Memor., Nyago Agric. Univ., 2: 53.
- NEWELL, T.G. (1970). Three biometrical genetic analyses of activity in the mouse. Jour. Comp. Physiol. Psychol., 70: 37-47.
- NIEHAUS, M.H. and R.C. PICKETT (1966). Heterosis and combining ability in *Sorghum vulgare* Pers. Crop Sci., 6: 33-36.
- NIELSON, A.K. and R.R. KALTON (1959). Combining ability for seed characteristics in *Bromus inermis* Leyss. Agron. Jour., 51: 178-181.

- NORINGTON-DAVIES, J. (1967). Application of diallel analysis to experiments in plant competition. *Euphytica*, 16: 391-406.
- NORINGTON-DAVIES, J. (1968). Diallel analysis of competition between grass species. *Jour. Agric. Sci., Camb.*, 71: 223-231.
- PARODA, R.S. and J.D. HAYES (1971). An investigation of genotype-environment interactions for rate of ear emergence in spring barley. *Heredity*, 26: 157-175.
- PARODA, R.S. and A.B. JOSHI (1970). Genetic architecture of yield and components of yield in wheat. *Ind. Jour. Genet. Plant breed.*, 30: 298-314.
- PARODA, R.S. and A.B. JOSHI (1970a). Combining ability in wheat. *Ind. Jour. Genet. Plant breed.*, 30: 630-637.
- PARODI, R.C., F.L. PATTERSON and W.E. NYQUIST (1970). A six-parent diallel cross analysis of coleoptile elongation in wheat (*Triticum aestivum* L.). *Crop Sci.*, 578-580.
- PARSONS, P.A. and R.W. ALLARD (1960). Seasonal variation in lima bean seed size: An example of genotype-environment interaction. *Heredity*, 14: 115-123.
- PERKINS, J.M. (1970). Environmental and genotype-environmental component of variability. VI. Diallel sets of crosses. *Heredity*, 25: 29-40.
- PERKINS, J.M. and J.L. JINKS (1970). Detection and estimation of genotype-environmental, linkage and epistatic components of variation for a metrical trait. *Heredity*, 25: 157-177.
- PERKINS, J.M. and J.L. JINKS (1971a). Analysis of genotype-environment interaction in triple test cross data. *Heredity*, 26: 203-209.
- PERKINS, J.M. and J.L. JINKS (1971b). Specificity of the interaction of genotypes with contrasting environments. *Heredity*, 26: 463-474.
- PERSSON, G. (1969). Diallel analysis of ear internode length in barley. *Hereditas*, 63: 39-47.
- PONELEIT, C.G. and L.F. BAUMAN (1970). Diallel analysis of fatty acid in corn (*Zea mays* L.) oil. *Crop Sci.*, 10: 338-341.
- PORCEDDU, D.E. (1968). Environmental component and genotype x environmental interaction in plant breeding work. Publication of Institute of Agric. Ecology, The Univ. of Perugia, Italy, 13 pp.

- POVILAITIS, B. (1966). Diallel cross analysis of quantitative characters in tobacco. *Can. Jour. Genet. Cytol.*, 8: 336-346.
- POVILAITIS, B. (1970). Diallel analysis of crosses between flue-cured and burley tobacco varieties. *Can Jour. Genet. Cytol.*, 12: 484-489.
- QUALSET, C.O. (1968). Genotype-environment interaction for awn development in isogenic lines of barley. *Theoret. Appl. Genetics*, 38: 355-360.
- RIGGS, T.J. and A.M. HAYTER (1972). Diallel analysis of the time-to-heading in spring barley. *Heredity*, 29: 341-357.
- RIGGS, T.J. and A.M. HAYTER (1973). Diallel analysis of number of grains per ear in spring barley. *Heredity*, 31: 95-105.
- RILEY, R., G. KIMBER and V. CHAPMAN (1961). Origin of genetic control of diploid-like behaviour of polyploid wheat. *Jour. Heredity*, 52: 22-25.
- RILEY, R., J. UNRAU and V. CHAPMAN (1958). Evidence on the origin of B genome of wheat. *Jour. Hered.*, 49: 91-98.
- SARKAR, P. and G.L. STEBBINS (1956). Morphological evidence concerning the origin of the B genome in wheat. *Amer. Jour. Bot.*, 43: 297-304.
- SCHEFFE, H. (1959). The analysis of variance. John Wiley and Sons, New York, 477 pp.
- SCHMIDT, J. (1919). La valeur de l'individu a titre de generateur appreciees suivant le methode du croisement diallele. *C.R. Lab., Clasberg*, 14: 1-33.
- SEARS, E.R. (1948). The cytology and genetics of the wheat and their relatives. *Advances in Genet.*, 2: 239-270.
- SEARS, E.R. and M. OKAMOTO (1958). Intergenomic chromosome relationships in hexaploid wheats. *Proceedings, 10th. Intern. Congress of Genetics*, 2: 258-259.
- SINGH, K.B., D. SHARMA and P.D. MEHNDIRATTA (1969). Study of combining ability and genetic parameters for yield and its components in wheat. *Japanese Jour. Genet.*, 44: 367-377.
- SMOCEK, J. (1969). A contribution to the analysis between economic yield components and four morpho-physiological subcharacters in wheat. *Biologia Pl.*, 11: 260-269.

- SOOMRO, B.A. (1967). Combining ability in *Gossypium arboreum* L. M.Sc. Agriculture Thesis, University of Sind, Hyderabad, Pakistan.
- SOOMRO, B.A. and M.A. BALUCH (1969). Combining ability in *Gossypium arboreum* L. Yield of seed cotton. Pakistan Cottons, 13: 78-91.
- SPANGELO, L.P.S., R. WATKINS, C.S. HSU and S.O. FEJER (1971). Combining ability analysis in cultivated strawberry. Can. Jour. Pl. Sci., 51: 377-383.
- SPRAGUE, G.F. (1964). Estimates of genetic variances in two open pollinated varieties of maize and their reciprocal F₁ hybrids. Crop Sci., 4: 332-333.
- SPRAGUE, G.F. and W.T. FEDERER (1951). A comparison of variance components in corn yield trials. II. Error, year x variety, location x variety and variety components. Agron. Jour., 43: 535-541.
- SPRAGUE, G.F. and L.A. TATUM (1942). General versus specific combining ability in single crosses of corn. Jour. Amer. Soci. Agron., 34: 923-972.
- THEURER, J.C. and L.J. ELLING (1963a). Comparative performance of diallel crosses and related second generation synthetics of alfalfa. I. Bacterial wilt resistance. Crop Sci., 3: 50-53.
- THEURER, J.C. and L.J. ELLING (1963b). Comparative performance of diallel crosses and related second generation synthetics of alfalfa. II. Winter hardiness and resistance. *Ibid.* 3: 245.
- TROYER, A.F. and A.R. HALLAUER (1968). Analysis of a diallel set of early flint varieties of maize. Crop Sci., 8: 581-584.
- TURNER, J.H. (1953). A study of heterosis in upland cottons. I. Yield of hybrids compared with varieties. Agron. Jour., 45: 484-486.
- WALKER, J.T. (1963). Multiline concept and intervarietal heterosis. Empire Cotton Growing Review, 40(3): 190-215.
- WALTON, P.D. (1969). Inheritance of morphological characters associated with yield in spring wheat. Can. Jour. Plant Sci., 49: 587-596.
- WATKINS, R. and L.P.S. SPANGELO (1968). Components of genetic variance in cultivated strawberry. Genetics, 59: 93-103.

- WESTERMAN, J.M. (1970). Genotype-environment interaction and developmental regulation in *Arabidopsis thaliana*. II. Inbred lines; analysis. *Heredity*, 26: 93-106.
- WESTERMAN, J.M. (1971a). Genotype-environment interaction and developmental regulation in *Arabidopsis thaliana*. III. Inbred lines; analysis of response to photoperiod. *Heredity*, 26: 373-382.
- WESTERMAN, J.M. (1971b). Genotype-environment interaction and developmental regulation in *Arabidopsis thaliana*. IV. Wild material; analysis. *Heredity*, 26: 383-395.
- WHITE, T.G. and R.J. KOHEL (1964). A diallel analysis of agronomic characters in selected lines of cottons, *Gossypium hirsutum* L. *Crop Sci.*, 4: 254-257.
- WHITE, T.G. and T.R. RICHMOND (1963). Heterosis and combining ability in top and diallel crosses among primitive, foreign and cultivated American upland cottons. *Crop Sci.*, 3: 58-63.
- WHITEHOUSE, R.N.H., J.B. THOMPSON and M.A.M. DOVALLE PIPEIRO (1958). Studies on the breeding of self pollinated cereals. II. The use of diallel cross analysis in yield prediction. *Euphytica*, 7: 147-169.
- WIEBEL, D.E. (1956). Inheritance of quantitative characters in wheat. *Iowa State College, Jour. Sci.*, 30: 450-451.
- WILCOX, J.B. and C.P. WILSIE (1964). Estimated general and specific combining ability effects and reciprocal effects in crosses among nine clones of alfalfa, *Medicago sativa* L. *Crop Sci.*, 4: 375-377.
- WRIGHT, S. (1952). The genetics of quantitative variability. In Reeve, E.C.R. and C.H. WADDINGTON (Editors), *Quantitative Inheritance*. Her Majesty's Stationary Office, London, page 5-40.
- WU, H.P. (1968a). Studies on quantitative inheritance of *Oriza sativa* L. I. A diallel analysis of heading time and plant height in F₁ progeny. *Bot. Bull., Academia Sinica*, 9: 1-9.
- WU, H.P. (1968b). Studies on quantitative inheritance of *Oriza sativa* L. II. A diallel analysis of panicle number, tiller number, panicle length, spikelet number and number of primary branches in F₁ progeny. *Bot. Bull., Academia Sinica, (New Series)*, 9: 124-138.

- YAP, T.C. and B.L. HARVEY (1971). Heterosis and combining ability of barley hybrids in densely and widely seeded conditions. Can. Jour. Plant Sci., 51: 115-122.
- YATES, F. (1947). Analysis of data from all possible reciprocal crosses between a set of parental lines. Heredity, 1: 287-301.
- ZOHARY, D. and M. FELDMAN (1962). Hybridization between amphidiploids and the evolution of polyploids in wheat (*Aegilops-Triticum*) group. Evolution, 16: 44-61.

APPENDIX I

Origin, parentage and varietal description of five cultivars of wheat used in diallel study

Variety: Marquis
Origin: Central Experimental Farm, Ottawa, Canada
Parents: Hard Red Calcutta x Red Fyfe
Growth habit: Spring
Plant height: 110 - 120 cms.
Spike: Mid-long, fusiform with apical awns; beaks short, acute
Kernel: Dark red, hard, ovate-truncate

Variety: Chinook
Origin: Central Experimental Farm, Ottawa, Canada
Parents: Thatcher x S-615-11
Growth habit: Spring
Plant height: 110 - 125 cms.
Spike: Fusiform, mid-long, short apical awns, white glumes
with mid-wide beaks
Kernel: Red, hard, short to mid-long, oval

Variety: Khush-hal
Origin: Agricultural Research Institute, Peshawar, Pakistan
Parents: Local white x Standard Desi
Growth habit: Spring
Plant height: 80 - 90 cms.
Spike: White, flufy, awned; white pubiscent glumes with
mid-wide beaks
Kernel: Amber colored, soft, mid-long, oval

Variety: Ciano-67
Origin: National Institute of Agricultural Research, Mexico
Parents: Pitic 62-Chris 'Sib' x Sonora 64
Growth habit: Spring
Plant height: 85 - 95 cms.
Spike: White, bearded, fusiform
Kernel: Hard red, medium size

Variety: Inia-66
Origin: National Institute of Agricultural Research, Mexico
Parents: Lerma Rojo 64 x Sonora 64
Growth habit: Spring
Plant height: 100 - 110 cms.
Spike: White, bearded, fusiform
Kernel: Hard, red, medium-long

APPENDIX--II

NUMERICAL DESIGNATIONS OF THE PARENTS AND THEIR CROSSES USED IN THE DIALLEL ANALYSES

1. (KxCH)F22	46. (CHxI)I1	91. I-PARENT	136. K1 (CxK)	181. (CxK)F2
2. (IxK)I1	47. C-PARENT	92. (CxK)C1	137. (MxCH)M1	182. (IxK)F22
3. I1 (IxK)	48. (CxK)F22	93. CH0 (MxCH)	138. (CxI)F2	183. CH0 (CHxC)
4. (KxM)F22	49. (CHxI)CH0	94. CH1 (CxCH)	139. IO (KxI)	184. (IxCH)I1
5. (IxK)I1	50. (KxI)I1	95. C1 (CxM)	140. CO (MxC)	185. (CHxC)C1
6. (CxI)F22	51. (CHxI)F2	96. (IxM)I1	141. (CHxK)F1	186. IO (IxM)
7. CH1 (MxCH)	52. C1 (IxK)	97. (MxCH)CH1	142. (IxK)C1	187. IO (CHxI)
8. (IxK)F2	53. (KxM)K0	98. M1 (CxM)	143. M1 (IxM)	188. (KxC)CO
9. M-PARENT	54. (KxM)M0	99. (CxCH)CH1	144. CO (KxC)	189. (IxCH)F1
10. K1 (KxCH)	55. M0 (MxC)	100. (CxCH)F2	145. (CHxC)F2	190. (KxI)IO
11. (CxI)C1	56. (MxI)F22	101. CO (IxK)	146. K0 (IxK)	191. CO (CHxC)
12. (MxK)M0	57. IO (IxK)	102. K1 (KxI)	147. (CxM)C1	192. (CxM)CO
13. K1 (CHxK)	58. (MxC)CO	103. (KxC)K0	148. (MxCH)F22	193. (KxM)F1
14. (CHxM)CH1	59. (CHxM)F2	104. (MxC)F22	149. K0 (CxK)	194. (CHxK)CH0
15. C1 (CHxC)	60. CH1 (CHxM)	105. (KxCH)CH0	150. (MxI)F1	195. (IxM)IO
16. K-PARENT	61. (CHxC)F22	106. C1 (MxC)	151. (KxI)F2	196. (IxCH)IO
17. (IxK)K1	62. M0 (CHxM)	107. CH-PARENT	152. CH1 (KxCH)	197. CH0 (KxCH)
18. CH1 (CHxK)	63. (MxC)F2	108. C1 (CxK)	153. CO (CxCH)	198. M1 (MxK)
19. (KxCH)F2	64. M0 (IxM)	109. (CHxK)CH1	154. (MxI)M0	199. IO (IxK)
20. CH1 (CHxC)	65. (IxCH)CH0	110. (MxCH)M0	155. M1 (CHxM)	200. (MxC)M0
21. (MxK)M1	66. (KxI)F22	111. M1 (MxCH)	156. K0 (MxK)	201. I1 (CHxI)
22. I1 (IxK)	67. (CxM)M0	112. (MxI)M1	157. (MxCH)CH0	202. (KxI)K0
23. C1 (CxCH)	68. (CxI)CO	113. (CxM)F2	158. (MxCH)F1	203. (CxK)CO
24. (KxC)F2	69. (KxC)C1	114. (CHxM)CH0	159. K1 (IxK)	204. (IxK)F1
25. (MxK)F22	70. (CxCH)CH0	115. (IxK)F1	160. (IxK)CO	205. (CHxC)F1
26. (IxK)F22	71. M1 (MxC)	116. (CHxK)K0	161. (CxM)M1	206. I1 (IxCH)
27. (CHxC)CH1	72. K0 (KxI)	117. (CHxI)F22	162. CO (CxM)	207. K0 (KxCH)
28. CH1 (CHxI)	73. (CHxI)CH1	118. (IxK)IO	163. CH0 (CHxK)	208. M0 (CxM)
29. I1 (KxI)	74. (CxK)K1	119. I1 (MxI)	164. (KxI)K1	209. (IxK)IO
30. (IxCH)CH1	75. (MxI)IO	120. M1 (KxM)	165. CH0 (CHxI)	210. (CHxK)F22
31. K1 (KxC)	76. (CHxM)M1	121. (MxC)C1	166. M1 (MxI)	211. (CHxI)IO
32. (CxI)I1	77. (CxCH)C1	122. (IxM)M1	167. CO (CxK)	212. CH0 (CxCH)
33. (CxK)F1	78. (CHxM)F22	123. CH0 (CHxM)	168. (CxM)F1	213. K1 (KxM)
34. CH1 (IxCH)	79. IO (MxI)	124. (KxM)K1	169. (KxM)F2	214. (CxK)K0
35. (CHxC)CO	80. (MxCH)F2	125. (IxM)F1	170. IO (IxCH)	215. (KxI)F1
36. K0 (KxM)	81. M0 (KxM)	126. M0 (MxK)	171. K1 (MxK)	216. (MxC)F1
37. (IxM)F2	82. (KxCH)K1	127. (MxC)M1	172. (IxK)F2	217. M0 (MxI)
38. (CHxK)K1	83. IO (CxI)	128. I1 (IxM)	173. (CxI)F1	218. K0 (KxC)
39. (IxK)K0	84. (MxK)F2	129. (MxI)F2	174. M0 (MxCH)	219. CO (CxI)
40. (KxM)M1	85. (CxCH)F1	130. K0 (CHxK)	175. (CxCH)F22	220. (MxK)F1
41. (KxC)F1	86. (CHxM)M0	131. (IxCH)F2	176. (CHxM)F1	221. (CxCH)CO
42. (KxC)F22	87. (IxCH)F22	132. (KxC)K1	177. (MxI)I1	222. (CxI)IO
43. (CHxK)F2	88. CH0 (IxCH)	133. C1 (CxI)	178. (KxCH)CH1	223. (KxCH)F1
44. (CHxC)CH0	89. (MxK)K1	134. (CxM)F22	179. I1 (CxI)	224. (KxCH)K0
45. (IxM)M0	90. (IxM)F22	135. C1 (KxC)	180. (MxK)K0	225. (CHxI)F1

NOTE: M=Marquis, CH=Chinook, K=Khush-hal, C=Ciano-67 and I=Inia-66.

Taking any two varieties, for example 'C' and 'K', above mentioned combinations could be explained as follows:

(CxK)F1 = F₁ hybrid.
 (KxC)F1 = Reciprocal F₁ hybrid.
 (CxK)F2 = F₂-generation hybrid.
 (KxC)F2 = Reciprocal F₂ hybrid.
 (CxK)F22 and its reciprocal are the F₂'s repeated second time in each replication to complete the requirements of the 15x15 partially balanced lattice design.

(CxK)CO = Back cross-1.
 CO (CxK) = Reciprocal back cross.
 (CxK)K0 = Back cross-2.
 K0 (CxK) = Reciprocal back cross-2.
 (CxK)C1 = Selfed generation of (CxK)CO.
 C1 (CxK) = Reciprocal of (CxK)C1.
 (CxK)K1 = Selfed generation of (CxK)K0.
 K1 (CxK) = Reciprocal of (CxK)K1.

APPENDICES III TO XXII

Unadjusted treatment means (original data) of all the entries with respect to ten quantitative characters at two locations.

The numbers in the first row of each block are the code numbers of entries and those in the second row are the mean values of the corresponding entries listed in Appendix II .

ELLERSLIE REPLICATION-1.															
(block)	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115
1.	50.000	51.000	56.000	54.000	51.000	54.000	52.000	53.000	53.000	53.000	53.000	52.000	52.000	54.000	52.000
2.	52.000	52.000	57.000	52.000	53.000	54.000	51.000	53.000	52.000	52.000	52.000	52.000	55.000	54.000	55.000
3.	51.000	51.000	53.000	51.000	51.000	52.000	53.000	52.000	52.000	55.000	52.000	52.000	52.000	54.000	54.000
4.	51.000	49.000	51.000	53.000	52.000	53.000	49.000	51.000	54.000	55.000	52.000	52.000	51.000	52.000	57.000
5.	51.000	57.000	52.000	52.000	57.000	56.000	55.000	53.000	57.000	52.000	53.000	53.000	53.000	52.000	53.000
6.	54.000	54.000	54.000	52.000	53.000	55.000	57.000	53.000	54.000	53.000	53.000	51.000	52.000	53.000	52.000
7.	51.000	51.000	56.000	53.000	52.000	53.000	57.000	57.000	51.000	51.000	51.000	53.000	51.000	52.000	54.000
8.	53.000	56.000	51.000	53.000	52.000	52.000	52.000	50.000	51.000	51.000	56.000	52.000	54.000	50.000	52.000
9.	53.000	55.000	52.000	52.000	57.000	56.000	58.000	58.000	52.000	52.000	57.000	52.000	53.000	53.000	53.000
10.	54.000	52.000	52.000	53.000	51.000	51.000	55.000	51.000	60.000	52.000	50.000	54.000	52.000	59.000	52.000
11.	52.000	54.000	58.000	53.000	52.000	52.000	53.000	52.000	52.000	53.000	55.000	53.000	52.000	52.000	54.000
12.	53.000	51.000	51.000	56.000	52.000	54.000	53.000	53.000	54.000	57.000	53.000	50.000	53.000	52.000	55.000
13.	52.000	57.000	50.000	53.000	50.000	54.000	52.000	53.000	51.000	52.000	52.000	51.000	52.000	52.000	54.000
14.	58.000	51.000	57.000	51.000	57.000	55.000	55.000	51.000	52.000	54.000	59.000	52.000	53.000	52.000	54.000
15.	54.000	52.000	54.000	54.000	53.000	52.000	52.000	51.000	60.000	52.000	60.000	53.000	58.000	51.000	53.000

REPLICATION-2.															
	13	29	44	59	74	89	104	119	134	149	164	179	194	209	224
1.	53.000	54.000	51.000	57.000	52.000	53.000	54.000	52.000	53.000	52.000	52.000	52.000	56.000	52.000	56.000
2.	55.000	57.000	53.000	53.000	52.000	59.000	52.000	52.000	56.000	51.000	52.000	55.000	51.000	52.000	51.000
3.	60.000	52.000	53.000	56.000	50.000	54.000	54.000	57.000	53.000	52.000	57.000	54.000	52.000	51.000	51.000
4.	51.000	50.000	52.000	52.000	58.000	51.000	52.000	58.000	56.000	56.000	54.000	52.000	49.000	57.000	51.000
5.	53.000	57.000	55.000	55.000	53.000	54.000	53.000	58.000	54.000	54.000	54.000	54.000	53.000	53.000	53.000
6.	51.000	52.000	52.000	53.000	53.000	57.000	52.000	53.000	52.000	52.000	54.000	57.000	52.000	52.000	51.000
7.	50.000	53.000	56.000	53.000	52.000	53.000	52.000	51.000	53.000	53.000	52.000	52.000	52.000	54.000	55.000
8.	52.000	53.000	53.000	54.000	52.000	52.000	57.000	53.000	53.000	53.000	58.000	52.000	52.000	52.000	53.000
9.	51.000	54.000	52.000	52.000	53.000	57.000	57.000	52.000	59.000	51.000	52.000	52.000	52.000	59.000	54.000
10.	51.000	54.000	53.000	53.000	54.000	52.000	52.000	53.000	51.000	58.000	54.000	55.000	55.000	53.000	54.000
11.	56.000	53.000	52.000	52.000	52.000	53.000	53.000	53.000	52.000	53.000	54.000	53.000	53.000	53.000	52.000
12.	52.000	53.000	53.000	52.000	53.000	57.000	52.000	57.000	52.000	52.000	57.000	53.000	52.000	52.000	53.000
13.	55.000	55.000	53.000	53.000	54.000	52.000	53.000	54.000	52.000	52.000	52.000	53.000	53.000	52.000	52.000
14.	60.000	52.000	53.000	52.000	52.000	55.000	58.000	55.000	57.000	52.000	55.000	52.000	52.000	53.000	54.000
15.	52.000	55.000	53.000	59.000	53.000	53.000	58.000	53.000	52.000	54.000	52.000	53.000	53.000	53.000	54.000

REPLICATION-3.															
	45	59	73	87	101	115	129	143	157	171	185	199	213	2	16
1.	52.000	54.000	54.000	52.000	52.000	52.000	53.000	52.000	54.000	53.000	52.000	52.000	52.000	52.000	52.000
2.	53.000	54.000	53.000	52.000	52.000	54.000	59.000	52.000	53.000	53.000	52.000	52.000	57.000	58.000	54.000
3.	52.000	52.000	52.000	53.000	52.000	52.000	55.000	53.000	53.000	52.000	52.000	55.000	50.000	51.000	53.000
4.	53.000	52.000	55.000	54.000	52.000	57.000	55.000	53.000	52.000	53.000	57.000	53.000	52.000	55.000	54.000
5.	53.000	52.000	50.000	50.000	57.000	49.000	52.000	50.000	53.000	52.000	52.000	54.000	52.000	57.000	61.000
6.	54.000	54.000	56.000	52.000	50.000	54.000	52.000	53.000	57.000	57.000	52.000	52.000	58.000	57.000	53.000
7.	53.000	50.000	53.000	54.000	53.000	53.000	52.000	57.000	49.000	52.000	57.000	57.000	57.000	57.000	57.000
8.	50.000	52.000	53.000	51.000	53.000	52.000	53.000	52.000	57.000	52.000	54.000	53.000	52.000	54.000	52.000
9.	54.000	54.000	54.000	52.000	54.000	51.000	54.000	54.000	57.000	58.000	52.000	51.000	54.000	51.000	52.000
10.	52.000	51.000	53.000	53.000	52.000	52.000	52.000	52.000	53.000	53.000	50.000	52.000	58.000	52.000	58.000
11.	52.000	52.000	55.000	53.000	52.000	53.000	52.000	53.000	51.000	52.000	57.000	53.000	52.000	53.000	52.000
12.	54.000	52.000	55.000	52.000	58.000	52.000	52.000	52.000	57.000	57.000	52.000	54.000	54.000	52.000	52.000
13.	55.000	53.000	52.000	52.000	59.000	52.000	57.000	54.000	52.000	53.000	53.000	54.000	57.000	52.000	54.000
14.	52.000	53.000	53.000	55.000	52.000	55.000	54.000	52.000	53.000	52.000	54.000	56.000	56.000	52.000	55.000
15.	54.000	53.000	53.000	57.000	52.000	53.000	52.000	52.000	57.000	57.000	53.000	52.000	52.000	52.000	50.000

APPENDIX IV Final heading at Ellerslie

227

(Block)	ELLERSLIE REPLICATION-1.														
	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
1.	58.000	58.000	61.000	62.000	61.000	58.000	61.000	61.000	61.000	60.000	59.000	59.000	60.000	62.000	58.000
2.	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
3.	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225
4.	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
5.	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
6.	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135
7.	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
8.	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
9.	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165
10.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
11.	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210
12.	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
13.	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150
14.	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
15.	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180

REPLICATION-2.

1.	14	29	44	59	74	89	104	119	134	149	164	179	194	209	224
2.	1	16	31	46	61	76	91	106	121	136	151	166	181	196	211
3.	9	24	39	54	69	84	99	114	129	144	159	174	189	204	219
4.	2	17	32	47	62	77	92	107	122	137	152	167	182	197	212
5.	6	21	36	51	66	81	96	111	126	141	156	171	186	201	216
6.	11	26	41	56	71	86	101	116	131	146	161	176	191	206	221
7.	10	25	40	55	70	85	100	115	130	145	160	175	190	205	220
8.	8	23	38	53	68	83	98	113	128	143	158	173	188	203	218
9.	3	18	33	48	63	78	93	108	123	138	153	168	183	198	213
10.	13	28	43	58	73	88	103	118	133	148	163	178	193	208	223
11.	12	27	42	57	72	87	102	117	132	147	162	177	192	207	222
12.	5	20	35	50	65	80	95	110	125	140	155	170	185	200	215
13.	4	19	34	49	64	79	94	109	124	139	154	169	184	199	214
14.	7	22	37	52	67	82	97	112	127	142	157	172	187	202	217
15.	15	30	45	60	75	90	105	120	135	150	165	180	195	210	225

REPLICATION-3.

1.	45	59	73	87	101	115	129	143	157	171	185	199	213	2	16
2.	150	164	178	192	206	220	23	37	51	65	79	93	107	121	
3.	90	104	118	132	146	160	174	188	202	216	5	19	33	47	61
4.	195	209	223	12	26	40	54	68	82	96	110	124	138	152	166
5.	105	119	133	147	161	175	189	203	217	6	20	34	48	62	76
6.	180	194	208	222	11	25	39	53	67	81	95	109	123	137	151
7.	60	74	88	102	116	130	144	158	172	186	200	214	3	17	31
8.	15	29	43	57	71	85	99	113	127	141	155	169	183	197	211
9.	225	14	28	42	56	70	84	98	112	126	140	154	168	182	196
10.	135	149	163	177	191	205	219	8	22	36	50	64	78	92	106
11.	165	179	193	207	221	10	24	38	52	66	80	94	108	122	136
12.	120	134	148	162	176	190	204	218	7	21	35	49	63	77	91
13.	30	44	58	72	86	100	114	128	142	156	170	184	198	212	1
14.	75	89	103	117	131	145	159	173	187	201	215	4	18	32	46
15.	210	224	13	27	41	55	69	83	97	111	125	139	153	167	181

APPENDIX V Heading-span at Ellerslie

228

REPLICATION-1															
(Block)	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
1.	8.000	7.000	5.000	8.000	10.000	7.000	9.000	8.000	8.000	7.000	7.000	7.000	6.000	8.000	6.000
2.	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
	10.000	8.000	7.000	10.000	9.000	10.000	7.000	6.000	8.000	9.000	7.000	7.000	8.000	6.000	10.000
3.	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225
	8.000	9.000	11.000	7.000	6.000	8.000	9.000	6.000	6.000	7.000	8.000	6.000	7.000	7.000	8.000
4.	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
	8.000	8.000	7.000	8.000	6.000	7.000	9.000	8.000	8.000	7.000	8.000	7.000	8.000	8.000	10.000
5.	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
	12.000	7.000	7.000	10.000	8.000	8.000	7.000	10.000	10.000	8.000	8.000	8.000	7.000	8.000	8.000
6.	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135
	8.000	9.000	11.000	9.000	7.000	8.000	8.000	6.000	8.000	8.000	8.000	9.000	7.000	7.000	8.000
7.	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
	8.000	8.000	10.000	8.000	7.000	5.000	6.000	6.000	11.000	7.000	7.000	7.000	8.000	6.000	8.000
8.	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
	5.000	9.000	8.000	7.000	7.000	6.000	10.000	8.000	8.000	8.000	8.000	8.000	9.000	10.000	7.000
9.	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165
	8.000	9.000	11.000	11.000	10.000	9.000	7.000	7.000	9.000	7.000	7.000	8.000	8.000	6.000	8.000
10.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
	10.000	7.000	6.000	9.000	7.000	7.000	9.000	7.000	7.000	7.000	6.000	10.000	8.000	7.000	6.000
11.	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210
	12.000	7.000	9.000	6.000	11.000	8.000	6.000	7.000	7.000	7.000	6.000	9.000	9.000	7.000	10.000
12.	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
	9.000	6.000	6.000	11.000	7.000	9.000	9.000	7.000	9.000	7.000	5.000	10.000	9.000	13.000	9.000
13.	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150
	7.000	9.000	10.000	7.000	9.000	8.000	6.000	8.000	8.000	9.000	6.000	7.000	9.000	6.000	7.000
14.	75	77	78	79	80	81	82	83	84	85	86	87	88	89	90
	8.000	8.000	8.000	6.000	7.000	9.000	9.000	8.000	9.000	7.000	7.000	8.000	7.000	8.000	6.000
15.	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180
	9.000	6.000	6.000	8.000	7.000	8.000	6.000	7.000	7.000	7.000	7.000	10.000	9.000	8.000	11.000

REPLICATION-2															
	19	29	44	59	74	89	104	119	134	149	164	179	194	209	224
1.	11.000	6.000	9.000	10.000	7.000	7.000	6.000	7.000	6.000	6.000	7.000	6.000	7.000	7.000	8.000
2.	1	16	31	46	61	76	91	106	121	136	151	166	181	196	211
	9.000	6.000	12.000	10.000	10.000	6.000	6.000	9.000	6.000	7.000	7.000	12.000	7.000	7.000	8.000
3.	9	24	39	54	69	84	99	114	129	144	159	174	189	204	219
	8.000	6.000	7.000	8.000	8.000	7.000	8.000	9.000	7.000	5.000	6.000	9.000	8.000	6.000	6.000
4.	2	17	32	47	62	77	92	107	122	137	152	167	182	197	212
	10.000	9.000	6.000	7.000	8.000	8.000	7.000	8.000	7.000	7.000	8.000	6.000	9.000	7.000	9.000
5.	6	21	36	51	66	81	96	111	126	141	156	171	186	201	216
	7.000	10.000	7.000	7.000	5.000	11.000	7.000	7.000	8.000	6.000	8.000	9.000	6.000	7.000	6.000
6.	11	26	41	56	71	86	101	116	131	146	161	176	191	206	221
	7.000	6.000	5.000	8.000	8.000	8.000	6.000	7.000	7.000	7.000	8.000	7.000	8.000	7.000	9.000
7.	10	25	40	55	70	85	100	115	130	145	160	175	190	205	220
	11.000	11.000	9.000	8.000	9.000	7.000	7.000	7.000	7.000	7.000	5.000	7.000	7.000	6.000	7.000
8.	8	23	38	53	68	83	98	113	128	143	158	173	188	203	218
	6.000	6.000	6.000	9.000	6.000	6.000	7.000	9.000	6.000	8.000	9.000	6.000	6.000	6.000	7.000
9.	3	18	33	48	63	78	93	108	123	138	153	168	183	198	213
	7.000	7.000	6.000	6.000	7.000	7.000	8.000	6.000	5.000	7.000	8.000	7.000	8.000	8.000	9.000
10.	13	28	43	58	73	88	103	118	133	148	163	178	193	208	223
	9.000	10.000	9.000	6.000	8.000	8.000	8.000	6.000	7.000	9.000	13.000	10.000	9.000	11.000	8.000
11.	12	27	42	57	72	87	102	117	132	147	162	177	192	207	222
	9.000	12.000	7.000	6.000	7.000	8.000	8.000	8.000	9.000	6.000	8.000	9.000	9.000	9.000	7.000
12.	3	20	35	50	65	80	95	110	125	140	155	170	185	200	215
	7.000	13.000	7.000	8.000	8.000	9.000	7.000	8.000	7.000	10.000	10.000	7.000	7.000	8.000	5.000
13.	4	19	34	49	64	79	94	109	124	139	154	169	184	199	214
	9.000	9.000	11.000	11.000	6.000	7.000	6.000	10.000	12.000	7.000	10.000	7.000	8.000	7.000	6.000
14.	7	22	37	52	67	82	97	112	127	142	157	172	187	202	217
	7.000	7.000	7.000	5.000	9.000	7.000	9.000	10.000	8.000	6.000	10.000	7.000	7.000	8.000	7.000
15.	15	30	45	60	75	90	105	120	135	150	165	180	195	210	225
	5.000	10.000	7.000	9.000	6.000	6.000	8.000	7.000	6.000	8.000	7.000	9.000	6.000	7.000	6.000

REPLICATION-3.															
	45	59	73	87	101	115	129	143	157	171	185	199	213	2	16
1.	7.000	7.000	7.000	7.000	5.000	6.000	8.000	8.000	8.000	7.000	7.000	8.000	8.000	10.000	10.000
2.	150	164	178	192	206	220	234	248	262	276	290	304	318	332	346
	7.000	6.000	7.000	8.000	7.000	8.000	8.000	7.000	5.000	7.000	8.000	8.000	8.000	8.000	6.000
3.	90	104	118	132	146	160	174	188	202	216	230	244	258	272	286
	6.000	8.000	6.000	7.000	5.000	6.000	12.000	7.000	6.000	6.000	7.000	5.000	8.000	6.000	6.000
4.	195	209	223	237	251	265	279	293	307	321	335	349	363	377	391
	6.000	6.000	7.000	9.000	7.000	6.000	8.000	7.000	6.000	6.000	11.000	8.000	6.000	5.000	8.000
5.	105	119	133	147	161	175	189	203	217	231	245	259	273	287	301
	11.000	7.000	7.000	8.000	8.000	9.000	7.000	9.000	7.000	8.000	9.000	11.000	7.000	10.000	3.000
6.	190	194	208	222	236	250	264	278	292	306	320	334	348	362	376
	6.000	6.000	6.000	6.000	7.000	7.000	9.000	7.000	7.000	7.000	7.000	8.000	10.000	8.000	7.000
7.	60	74	88	102	116	130	144	158	172	186	200	214	228	242	256
	10.000	8.000	6.000	6.000	7.000	7.000	5.000	8.000	9.000	6.000	10.000	5.000	4.000	6.000	5.000
8.	15	29	43	57	71	85	99	113	127	141	155	169	183	197	211
	9.000	7.000	7.000	6.000	7.000	7.000	7.000	7.000	7.000	8.000	7.000	7.000	8.000	6.000	8.000
9.	225	239	253	267	281	295	309	323	337	351	365	379	393	407	421
	6.000	9.000	7.000	7.000	8.000	8.000	7.000	8.000	8.000	9.000	7.000	7.000	6.000	7.000	6.000
10.	135	149	163	177	191	205	219	233	247	261	275	289	303	317	331
	7.000	8.000	8.000	7.000	7.000	8.000	6.000	6.000	5.000	7.000	8.000	7.000	8.000	7.000	5.000
11.	155	179	193	207	221	235	249	263	277	291	305	319	333	347	361
	7.000	7.000	7.000	11.000	7.000	10.000	6.000	9.000	7.000	6.000	8.000	6.000	6.000	9.000	7.000
12.	120	134	148	162	176	190	204	218	232	246	260	274	288	302	316
	8.000	10.000	9.000	9.000	8.000	7.000	5.000	6.000	7.000	8.000	7.000	8.000	6.000	7.000	6.000
13.	30	44	58	72	86	100	114	128	142	156	170	184	198	212	226
	10.000	8.000	8.000	7.000	10.000	7.000	8.000	5.000	6.000	7.000	6.000	6.000	7.000	8.000	11.000
14.	75	89	103	117	131	145	159	173	187	201	215	229	243	257	271
	7.000	8.000	6.000	9.000	8.000	5.000	5.000	6.000	6.000	8.000	5.000	6.000	7.000	6.000	10.000
15.	210	224	238	252	266	280	294	308	322	336	350	364	378	392	406
	8.000	7.000	9.000	7.000	6.000	10.000	7.000	6.000	7.000	7.000	6.000	6.000	6.000	6.000	7.000

(Block)	EXPOSURE				REPLICATION-1.				PLANT HEIGHT							
	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	
1.	72.500	67.900	105.330	85.050	85.450	71.340	95.010	90.340	93.480	80.350	101.590	111.240	103.210	95.390	78.210	
	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	
2.	74.450	74.270	110.130	91.200	103.680	111.300	69.420	87.410	76.870	101.380	75.450	112.980	109.400	75.730	106.920	
	211	212	211	214	215	216	217	218	219	220	221	222	223	224	225	
3.	83.980	84.550	88.570	72.500	71.890	84.940	103.180	71.490	75.280	96.550	98.540	73.750	93.510	97.480	92.160	
	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	
4.	95.430	81.800	79.170	116.920	93.400	104.770	06.200	114.900	122.340	91.230	101.300	78.220	104.620	125.310	120.860	
	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	
5.	101.750	105.530	74.810	97.060	120.020	115.310	105.510	87.990	110.540	69.282	82.650	92.050	75.900	81.050	92.850	
	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	
6.	95.030	94.260	106.900	83.390	04.360	94.270	110.810	75.930	97.450	86.480	82.590	77.350	77.870	85.030	70.360	
	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	
7.	70.700	75.620	116.660	99.500	82.620	76.620	115.050	104.980	57.180	90.570	72.900	76.180	76.340	90.160	96.730	
	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	
8.	39.000	115.210	84.980	93.620	78.320	72.500	106.230	73.770	71.380	94.830	99.110	74.090	103.520	71.160	04.050	
	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	
9.	66.680	95.580	99.150	105.730	108.470	103.900	108.200	114.150	69.270	71.270	101.370	101.490	89.360	74.940	89.430	
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	
10.	90.030	70.920	64.020	93.670	71.320	73.570	108.270	71.370	111.930	73.550	70.390	108.860	83.360	112.790	84.680	
	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	
11.	100.650	80.700	100.200	82.750	85.850	76.400	67.100	67.050	69.500	86.700	78.520	77.830	87.570	64.120	87.350	
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	
12.	69.200	66.970	66.900	87.400	74.200	92.300	70.320	82.090	73.730	101.550	70.250	73.000	92.260	102.420	91.220	
	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	
13.	67.130	101.290	68.330	65.720	91.320	91.270	67.010	97.570	72.440	89.540	73.160	75.430	102.220	72.630	92.730	
	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	
14.	108.040	78.390	103.770	77.750	105.990	93.500	75.830	75.950	87.440	96.300	100.340	86.770	78.020	77.020	74.125	
	156	167	168	169	170	171	172	173	174	175	176	177	178	179	180	
15.	97.750	69.500	90.940	68.970	97.050	90.470	72.840	71.790	111.350	80.570	111.040	82.610	98.180	72.650	81.110	

REPLICATION-2.

	14	27	44	59	74	89	104	119	134	149	164	179	194	209	224	
1.	108.160	71.220	100.150	112.410	76.630	83.940	94.860	93.180	96.460	75.160	80.700	78.440	89.000	73.440	99.010	
	1	16	31	46	61	76	91	106	121	136	151	166	181	196	211	
2.	89.020	73.810	83.980	104.460	99.320	118.230	74.440	111.580	125.470	74.120	76.660	102.760	72.410	101.200	89.430	
	9	24	39	54	69	84	99	114	129	144	159	174	189	204	219	
3.	124.420	80.020	77.080	103.780	79.820	108.730	107.750	123.290	53.390	79.760	79.050	121.340	102.190	78.670	70.500	
	2	17	32	47	62	77	92	107	122	137	152	167	182	197	212	
4.	69.470	66.140	73.500	76.440	110.950	78.270	112.280	97.890	93.030	110.000	107.040	73.490	73.980	100.580	107.180	
	6	21	36	51	66	81	96	111	126	141	156	171	186	201	216	
5.	73.580	112.290	90.730	134.770	68.640	95.370	87.510	123.500	112.810	103.930	99.390	103.780	89.200	96.140	96.820	
	11	26	41	56	71	86	101	116	131	146	161	176	191	206	221	
6.	87.430	76.960	79.100	98.690	107.020	121.270	78.990	87.480	85.880	78.310	115.230	130.590	37.390	92.240	100.260	
	10	25	40	55	70	85	100	115	130	145	160	175	190	205	220	
7.	75.000	95.720	108.830	92.111	94.060	99.310	84.110	72.720	51.490	92.530	73.300	83.540	70.620	99.370	93.700	
	3	23	38	53	68	83	98	113	128	143	158	173	188	203	218	
8.	72.500	90.350	82.940	101.380	72.790	73.380	104.400	99.240	79.520	93.060	126.070	77.750	75.790	74.500	76.230	
	3	18	33	48	63	78	93	108	123	138	153	168	183	198	213	
9.	71.190	108.850	76.530	78.940	102.280	123.900	122.540	73.160	122.730	76.930	106.130	101.060	93.510	125.120	99.120	
	13	28	43	58	73	88	103	118	133	148	163	178	193	208	223	
10.	87.120	115.350	101.650	91.880	101.890	93.040	70.810	72.630	82.660	115.540	100.070	104.530	99.430	108.730	99.710	
	12	27	42	57	72	87	102	117	132	147	162	177	192	207	222	
11.	103.320	101.710	72.750	73.550	68.350	93.420	72.390	93.330	76.590	76.460	95.520	93.680	98.340	90.300	70.770	
	5	20	35	50	65	80	95	110	125	140	155	170	185	200	215	
12.	68.540	103.140	77.280	50.340	96.960	117.490	87.120	80.370	102.530	93.620	86.540	114.810	112.400	84.900	117.970	
	8	19	34	49	64	79	94	109	124	139	154	169	184	199	214	
13.	92.840	96.330	106.040	101.380	83.120	84.780	99.330	96.460	82.630	79.170	105.770	90.650	74.650	71.600	72.950	
	7	22	37	52	67	82	97	112	127	142	157	172	187	202	217	
14.	113.090	72.400	76.570	72.960	99.183	75.640	111.670	101.810	103.830	76.690	121.590	72.450	96.450	103.340	75.300	
	15	30	45	60	75	90	105	120	135	150	165	180	195	210	225	
15.	61.970	102.660	79.890	115.420	86.910	75.190	98.480	93.690	77.730	95.920	82.660	91.680	81.620	103.240	89.180	

REPLICATION-3.

	45	59	73	87	101	115	129	143	157	171	185	199	213	2	16
1.	88.270	118.480	113.270	90.050	81.070	79.350	100.280	93.020	122.800	90.960	87.240	76.950	93.020	74.240	75.200
	150	164	178	192	206	220	9	23	37	51	65	79	93	107	121
2.	105.300	80.640	109.880	93.450	94.910	110.890	129.090	93.340	84.510	104.850	109.060	105.060	124.120	119.520	106.680
	90	104	118	132	146	160	174	188	202	216	5	19	33	47	61
3.	78.350	90.690	74.020	81.140	81.910	76.020	117.370	74.425	73.720	97.190	80.490	100.420	79.680	79.130	94.640
	195	209	223	12	26	40	54	68	82	96	110	124	138	152	166
4.	80.130	75.660	103.310	105.910	73.720	115.570	107.080	83.261	76.220	93.260	123.280	93.670	80.630	109.470	114.800
	105	119	133	147	161	175	189	203	217	6	20	34	48	62	76
5.	113.110	91.760	75.920	91.600	113.340	93.760	106.920	83.240	112.620	86.590	116.590	113.760	93.320	122.880	121.410
	180	194	208	222	11	25	39	53	67	81	95	109	123	137	151
6.	110.340	107.010	117.090	81.890	74.440	107.720	78.370	87.430	115.140	92.120	94.730	101.290	125.070	114.670	76.450
	60	74	88	102	116	130	144	158	172	186	200	214	3	17	31
7.	118.530	77.070	88.840	77.420	93.240	96.260	79.790	122.330	74.010	86.880	107.210	77.850	82.170	77.740	80.680
	15	29	43	57	71	85	99	113	127	141	155	169	183	197	211
8.	90.930	77.080	104.010	76.240	118.390	105.160	109.130	104.960	117.250	106.280	124.700	105.640	107.030	96.020	98.580
	225	14	28	42	56	70	84	98	112	126	140	154	168	182	196
9.	99.410	123.240	122.730	85.970	117.070	119.390	105.800	116.700	116.500	123.490	96.600	106.600	109.580	79.520	90.840
	135	149	163	177	191	205	219	8	22	36	50	64	78	92	106
10.	79.430	78.610	100.340	99.560	93.060	106.850	80.260	78.150	78.310	104.210	85.100	106.400	123.110	90.830	113.080
	165	179	193	207	221	10	24	38	52	66	80	94	108	122	136
11.	81.900	71.280	101.360	112.730	97.110	92.240	74.460	94.840	78.160	83.550	125.040	110.260	79.180	100.730	80.040
	120	134	148	162	176	190	204	218	7	21	35	49	63	77	91
12.	97.880	100.650	126.290	95.370	125.160	75.190	83.240	77.080	121.230	113.180	86.760	116.270	100.820	105.200	75.110
	30	44	58	72	86	100	114	128	142	156	170	184	198	212	1
13.	98.540	88.390	99.920	77.760	115.940	83.900	111.520	79.740	72.660	93.940	78.930	86.120	109.590	86.740	94.800
	75	89	103	117	131	145	159	173	187	201	215	4	18	32	46
14.	83.520	91.790	77.120	101.820	92.520	97.690	73.500	74.750	99.910	93.710	76.400	94.330	105.910	71.100	109.440
	210	224	13	27	41	55	69	83	97	111	125	139	153	167	181
15.	94.810	92.080	90.980	115.220	73.300	101.230	81.320	91.760	120.690	119.270	93.750	83.380	94.720	81.370	81.170

APPENDIX VII Number of tillers per plant at Ellerslie

230

ELLERSLIE APPLICATION-1. NUMBER OF TILLERS PER PLANT															
(Block)	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
1.	12.300	7.700	10.600	11.500	12.000	9.700	9.700	10.500	11.400	12.500	11.200	9.800	10.000	11.500	10.500
2.	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
3.	10.700	9.000	15.400	11.300	12.300	9.200	8.300	9.700	10.200	10.700	8.200	11.800	12.100	9.400	12.000
4.	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225
5.	9.800	10.333	11.300	10.000	8.700	10.000	12.300	8.200	9.800	8.300	11.200	8.500	11.100	13.800	9.300
6.	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
7.	10.400	12.000	11.800	10.300	11.900	10.900	9.700	7.400	11.000	7.400	8.500	9.200	10.100	8.600	12.600
8.	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
9.	11.300	9.000	10.900	11.100	11.500	10.500	11.700	10.922	11.474	8.454	14.000	11.900	7.900	11.700	11.100
10.	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135
11.	15.600	11.900	11.100	12.300	11.200	11.500	11.500	10.900	12.900	14.000	12.100	14.100	11.000	8.300	12.400
12.	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
13.	10.900	11.500	10.100	12.300	11.500	8.900	12.900	12.100	13.400	11.800	9.500	12.000	14.300	12.000	11.400
14.	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
15.	10.200	14.000	9.800	10.300	8.300	9.000	12.500	12.500	10.200	11.800	9.500	8.700	11.300	9.000	10.800
16.	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165
17.	10.200	11.400	11.100	10.200	9.400	10.100	9.200	12.100	12.600	8.000	10.800	9.500	13.300	12.200	10.700
18.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
19.	12.500	9.000	9.000	10.500	9.400	8.250	8.800	8.000	9.800	9.700	10.600	11.400	12.100	13.200	10.600
20.	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210
21.	9.900	9.400	8.700	7.400	9.500	7.800	6.800	8.000	7.900	7.500	7.500	8.100	7.300	5.700	10.000
22.	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
23.	10.400	9.300	10.100	8.400	9.700	11.800	7.300	9.800	12.400	9.400	10.500	11.600	11.800	12.600	8.700
24.	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150
25.	9.600	8.200	9.800	8.300	10.300	13.000	7.000	10.100	9.000	8.100	7.700	8.600	9.100	7.600	7.500
26.	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
27.	10.300	9.400	12.200	6.400	9.300	7.100	8.600	8.400	9.600	8.800	10.500	9.000	7.500	7.600	8.625
28.	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180
29.	9.200	8.111	11.100	7.889	9.100	8.700	9.000	9.800	10.000	8.800	10.800	9.400	9.400	8.700	9.700

REPLICATION-2.

	14	29	44	59	74	89	104	119	134	149	164	179	194	209	224
1.	10.900	9.700	9.100	11.000	10.600	9.500	10.000	9.600	12.200	11.989	12.200	11.900	12.000	8.800	12.100
2.	1	16	31	46	61	76	91	106	121	136	151	166	181	196	211
3.	11.600	12.900	15.222	9.800	13.600	15.100	8.700	9.900	11.800	9.800	12.000	10.400	10.111	12.400	13.667
4.	9	24	39	54	69	84	99	114	129	144	159	174	189	204	219
5.	15.100	12.600	12.700	11.000	11.100	13.400	16.200	15.000	11.700	12.100	13.100	14.500	11.300	12.900	17.333
6.	2	17	32	47	62	77	92	107	122	137	152	167	182	197	212
7.	13.200	9.556	8.500	9.600	13.700	10.900	13.200	10.700	9.100	11.800	14.900	9.400	10.600	15.200	14.600
8.	6	21	36	51	66	81	96	111	126	141	156	171	186	201	216
9.	13.600	14.111	13.200	14.300	10.400	12.600	12.000	12.900	15.100	17.333	15.800	19.500	13.200	13.200	16.200
10.	11	26	41	56	71	86	101	116	131	146	161	176	191	206	221
11.	11.600	10.800	13.400	12.700	14.700	14.900	12.500	10.500	10.300	11.200	14.200	11.300	10.200	9.800	17.400
12.	10	25	40	55	70	85	100	115	130	145	160	175	190	205	220
13.	10.900	11.600	11.100	11.778	15.400	15.200	10.600	10.000	8.200	12.200	12.600	8.200	9.000	12.700	11.222
14.	8	23	38	53	68	83	98	113	128	143	158	173	188	203	218
15.	10.100	16.600	13.200	14.000	11.700	11.000	12.700	11.200	14.400	10.200	15.900	12.100	11.200	11.500	13.600
16.	3	18	33	48	63	78	93	108	123	138	153	168	183	198	213
17.	9.700	13.900	12.000	12.700	12.200	14.700	12.200	10.900	14.700	12.400	13.600	13.300	16.100	11.000	16.100
18.	13	28	43	58	73	88	103	118	133	148	163	178	193	208	223
19.	12.900	12.600	15.000	9.800	11.400	12.500	10.400	9.700	11.400	13.800	17.900	14.900	13.400	14.300	19.900
20.	12	27	42	57	72	87	102	117	132	147	162	177	192	207	222
21.	13.300	9.300	13.300	9.400	8.800	11.800	11.800	12.100	11.100	9.200	9.800	8.100	10.700	15.000	10.600
22.	5	20	35	50	65	80	95	215	200	185	170	155	140	125	110
23.	9.700	16.900	9.800	11.800	11.600	13.700	14.100	15.000	12.600	14.778	10.200	13.100	13.300	10.800	13.000
24.	8	19	34	49	64	79	94	109	124	139	154	169	184	199	214
25.	11.300	12.200	14.100	11.700	11.100	8.600	15.500	10.700	7.900	11.600	11.900	9.800	9.700	9.500	11.000
26.	7	22	37	52	67	82	97	112	127	142	157	172	187	202	217
27.	10.800	11.200	10.400	12.700	12.333	11.900	12.200	11.100	15.600	11.300	11.700	13.200	10.800	11.700	13.100
28.	15	30	45	60	75	90	105	120	135	150	165	180	195	210	225
29.	15.700	10.100	11.100	10.400	12.200	10.700	10.200	10.000	13.100	9.700	10.000	11.000	9.400	14.800	9.100

APPLICATION-3.

	45	59	73	87	101	115	129	143	157	171	185	199	213	2	16
1.	8.700	11.600	12.600	12.800	11.900	11.600	13.100	10.500	14.700	12.300	11.300	11.500	11.200	11.400	14.100
2.	150	164	178	192	206	220	9	23	37	51	65	79	93	107	121
3.	12.300	14.500	14.800	12.600	11.300	13.700	11.400	14.100	12.800	14.600	13.300	11.500	11.800	17.200	11.900
4.	90	104	118	132	146	160	174	188	202	216	5	19	33	47	61
5.	12.200	13.400	10.200	15.900	10.400	8.300	12.200	11.000	9.900	10.800	10.300	9.800	10.400	10.000	9.800
6.	195	209	223	12	26	40	54	68	82	96	110	124	138	152	166
7.	12.800	12.400	13.700	11.000	11.176	11.100	15.300	12.531	12.700	15.300	12.732	17.700	14.400	18.500	14.500
8.	105	119	133	147	161	175	189	203	217	6	20	34	48	62	76
9.	15.000	12.500	12.000	13.300	12.700	12.000	13.700	16.100	11.200	14.500	10.900	14.800	11.800	14.800	15.500
10.	180	194	208	222	11	25	39	53	67	81	95	109	123	137	151
11.	16.000	11.900	14.300	11.300	10.200	13.600	12.300	12.300	11.600	12.000	10.900	12.700	10.900	10.900	9.000
12.	60	74	88	102	116	130	144	158	172	186	200	214	3	17	31
13.	15.500	14.900	11.900	12.900	16.400	14.800	12.800	12.700	13.500	11.300	13.700	13.500	11.700	12.200	11.111
14.	15	29	43	57	71	85	99	113	127	141	155	169	183	197	211
15.	17.400	14.800	17.900	11.700	14.200	13.700	14.900	15.700	12.400	15.000	15.900	14.100	15.300	13.400	9.200
16.	225	14	28	42	56	70	84	98	112	126	140	154	168	182	196
17.	10.500	14.700	13.800	15.100	12.800	13.100	15.300	11.200	13.500	15.300	11.176	11.300	9.700	12.500	14.200
18.	135	149	163	177	191	205	219	8	22	36	50	64	78	92	106
19.	14.000	12.700	12.300	10.900	14.300	14.500	13.300	10.900	13.500	13.100	15.000	9.400	15.200	14.200	15.400
20.	165	179	193	207	221	10	24	38	52	66	80	94	108	122	136
21.	11.300	9.100	12.400	13.700	11.700	18.500	16.700	13.800	11.100	15.500	13.900	16.500	13.600	11.800	11.700
22.	120	134	148	162	176	190	204	218	7	21	35	49	63	77	91
23.	10.800	13.100	12.500	12.200	11.600	9.300	10.300	10.500	10.100	9.700	12.400	12.800	9.000	14.100	10.000
24.	30	44	58	72	86	100	114	128	142	156	170	184	198	212	1
25.	10.500	10.778	13.100	11.500	12.700	11.600	12.600	11.900	10.600	12.000	9.800	11.300	13.000	12.000	15.600
26.	75	89	103	117	131	145	159	173	187	201	215	4	18	32	46
27.	11.800	13.400	13.600	13.800	13.100	13.500	13.900	11.300	9.900	11.600	11.300	11.900	10.500	7.500	12.400
28.	210	224	13	27	41	55	69	83	97	111	125	139	153	167	181
29.	11.900	12.400	9.400	12.400	13.300	11.000	12.300	9.700	12.400	10.000	10.200	9.600	12.700	13.100	14.600

APPENDIX VIII Number of spikelets per spike at Ellerslie

BLOCK		REPLICATION-1. NUMBER OF SPIKELETS PER SPIKE													
(Block)	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
1.	11.533	13.000	14.333	15.100	13.700	14.400	15.633	13.500	14.711	12.933	14.300	13.967	10.381	13.733	14.933
2.	11.667	13.100	14.800	13.467	12.833	14.833	12.867	12.200	12.667	13.867	14.667	15.933	14.167	14.633	16.267
3.	11.333	13.407	13.933	13.567	13.633	12.800	14.967	14.033	14.367	15.333	13.267	14.500	13.733	14.733	13.733
4.	14.533	13.333	13.833	14.133	14.067	15.100	15.000	14.300	15.233	11.500	14.867	14.600	15.533	15.567	14.667
5.	14.300	14.567	13.733	16.500	15.467	16.367	15.600	13.975	15.311	12.486	13.000	13.900	13.800	13.267	13.300
6.	14.667	15.933	15.733	13.133	14.567	14.767	15.767	14.467	16.000	15.167	15.133	14.133	15.467	13.833	14.300
7.	14.733	12.833	16.667	15.733	13.400	15.133	14.833	14.033	17.600	15.100	12.400	14.133	15.133	13.267	14.967
8.	14.400	15.933	14.833	15.900	14.367	12.800	15.300	14.500	11.700	14.467	16.467	14.200	15.100	13.500	14.567
9.	12.667	13.733	15.000	15.133	15.133	16.833	15.600	15.167	14.133	11.933	16.433	15.233	14.300	13.133	15.200
10.	13.300	12.700	15.600	16.367	12.600	14.200	14.833	14.167	16.600	11.800	13.467	15.500	12.867	17.433	12.367
11.	12.567	13.633	14.433	11.367	15.067	12.067	11.033	13.433	12.167	12.100	12.733	12.900	13.267	11.100	12.500
12.	13.167	13.267	11.500	13.100	11.700	14.333	13.500	12.767	14.300	15.367	12.833	13.333	12.733	15.800	15.800
13.	13.300	15.633	13.467	13.467	14.000	13.433	12.967	17.567	13.067	12.900	13.500	13.067	16.533	13.167	13.967
14.	15.167	12.567	14.200	11.500	14.433	13.067	14.233	12.567	14.900	13.567	15.700	15.433	14.100	13.967	14.750
15.	15.100	11.741	14.500	12.593	12.567	14.667	13.933	14.333	15.933	12.600	15.200	12.933	15.833	11.533	13.733

BLOCK		REPLICATION-2.													
(Block)	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
1.	15.133	13.700	14.567	13.633	13.667	15.667	14.633	13.933	15.000	13.852	12.567	12.067	12.933	15.233	15.033
2.	13.967	13.633	14.296	12.433	13.100	14.000	14.900	14.633	15.133	12.333	12.000	16.167	11.519	12.733	12.037
3.	15.400	12.167	12.733	14.333	13.367	14.133	16.667	15.433	14.500	11.533	12.033	15.100	12.633	12.733	14.037
4.	12.833	13.481	12.867	12.633	15.200	12.815	12.467	13.500	13.067	15.200	14.567	11.233	13.067	14.733	14.367
5.	12.633	15.630	15.133	15.167	12.633	13.800	15.267	16.400	15.200	12.926	13.967	14.300	14.200	13.067	15.500
6.	13.733	11.600	12.133	15.333	14.633	16.633	12.833	13.033	13.133	14.633	14.467	15.167	12.500	12.700	14.267
7.	12.000	13.967	15.300	13.444	13.267	14.433	13.367	13.433	12.633	13.500	12.500	12.833	13.067	15.133	14.704
8.	13.067	13.900	12.000	15.133	11.296	12.633	14.600	13.533	13.833	14.100	15.200	12.267	13.167	13.100	14.233
9.	14.333	14.733	13.067	12.067	13.633	14.933	15.067	15.200	15.067	13.133	13.833	16.300	12.733	16.267	15.067
10.	13.133	16.267	13.267	11.700	15.600	15.067	12.200	13.467	12.967	16.233	15.967	12.600	13.133	15.267	14.733
11.	16.133	15.267	14.067	13.333	13.700	14.800	13.667	16.033	15.033	14.000	14.000	13.833	13.200	13.733	14.600
12.	15.033	16.033	12.933	14.967	14.333	16.700	14.067	14.067	13.600	15.556	14.333	16.367	14.200	13.633	14.500
13.	15.033	15.300	13.267	13.967	16.300	14.067	15.567	16.400	14.100	15.400	16.704	15.133	12.967	13.533	13.833
14.	15.933	14.467	14.500	13.296	15.611	12.533	12.433	15.267	16.867	14.000	17.133	13.600	14.833	17.200	14.267
15.	13.767	12.700	13.967	14.233	16.267	14.400	14.967	14.733	13.933	12.600	14.267	15.567	13.633	15.300	14.467

BLOCK		REPLICATION-3.													
(Block)	25	59	73	87	101	115	129	143	157	171	185	199	213	2	16
1.	13.800	12.933	15.300	15.267	14.867	12.633	14.900	13.433	16.167	13.567	13.467	13.600	13.667	14.467	13.267
2.	14.267	14.333	13.733	16.133	15.333	15.433	14.867	14.300	15.033	15.500	14.533	15.533	16.033	14.967	15.767
3.	14.767	14.900	14.200	12.900	13.767	12.800	15.133	13.292	13.167	13.900	15.057	12.700	12.233	13.500	15.100
4.	12.800	14.900	14.400	13.900	13.310	14.600	14.300	14.594	14.900	14.100	14.461	14.133	15.833	14.533	13.800
5.	14.267	15.367	13.867	14.633	14.867	13.967	15.133	14.067	14.233	14.267	15.767	13.833	13.067	15.867	15.833
6.	15.500	13.600	14.800	14.033	13.900	14.233	13.967	13.500	16.067	14.200	14.567	14.500	15.667	15.233	12.300
7.	16.400	14.333	15.600	14.400	14.300	15.400	14.533	12.367	15.767	15.300	14.233	14.233	14.733	15.367	14.111
8.	15.367	15.667	14.167	15.167	16.867	15.467	15.967	15.400	15.933	16.600	15.433	14.567	13.833	14.667	14.667
9.	15.467	13.700	14.700	14.267	16.967	16.100	15.600	16.167	15.733	16.933	14.343	12.700	11.867	15.667	16.367
10.	16.000	13.633	15.267	14.200	15.367	15.633	14.367	13.833	15.267	16.267	14.633	14.700	14.600	14.967	17.700
11.	15.033	13.567	15.600	15.467	14.100	13.400	14.733	13.933	14.733	14.800	14.133	14.967	14.533	16.367	14.067
12.	15.067	13.667	17.533	14.200	13.367	12.567	16.767	13.967	13.667	14.200	13.100	15.533	14.000	14.933	13.600
13.	14.033	14.667	16.300	14.633	14.633	13.667	16.267	15.167	13.500	15.267	13.533	12.433	17.667	13.400	15.433
14.	14.300	14.233	13.533	15.500	16.167	14.700	16.700	15.200	14.033	15.567	13.667	14.767	13.267	11.467	13.433
15.	14.000	14.967	13.767	17.100	14.767	16.167	14.267	14.833	16.400	15.233	15.267	14.433	14.533	14.233	15.267

APPENDIX IX Number of seeds per spike at Ellerslie

ELLERSLIE REPLICATION-1. NUMBER OF SEEDS PER SPIKE															
(Spike)	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
1.	44.667	49.833	44.667	57.433	44.667	49.133	49.033	36.967	48.600	40.700	44.667	51.933	42.190	44.500	57.367
2.	43.233	48.867	49.333	49.133	44.767	60.067	57.633	43.967	44.600	49.233	50.600	42.067	46.600	49.000	40.833
3.	52.967	38.813	52.467	43.833	47.667	50.300	59.433	43.300	46.333	52.067	37.600	49.333	43.167	43.333	50.867
4.	46.500	39.500	38.867	38.500	42.167	48.067	47.067	43.200	47.833	40.400	56.600	49.367	50.033	45.000	53.733
5.	49.267	43.867	43.300	50.567	53.933	54.667	62.800	46.203	44.134	47.746	42.833	49.733	44.067	50.300	45.000
6.	56.667	58.033	49.767	40.500	51.067	51.233	63.267	45.433	52.900	40.133	47.100	38.800	50.767	42.700	43.767
7.	50.667	47.533	52.067	52.167	46.933	53.900	40.867	44.400	51.533	43.933	48.567	46.167	44.400	48.167	45.200
8.	44.100	50.667	49.833	61.700	46.833	49.067	58.567	49.633	37.400	49.400	54.333	49.267	52.167	42.700	56.100
9.	47.733	47.700	47.133	50.900	49.033	55.133	47.000	52.833	49.867	43.733	58.900	52.633	42.700	45.033	44.133
10.	45.433	52.433	56.033	54.033	45.833	48.203	42.800	45.233	56.233	38.633	43.200	50.233	34.333	55.967	41.633
11.	47.833	49.100	57.667	44.333	48.400	47.067	42.733	45.533	50.467	45.067	47.767	42.533	49.133	44.267	43.667
12.	43.433	50.433	39.067	36.000	41.300	50.133	45.333	44.267	49.800	48.933	37.500	42.467	42.133	47.133	61.000
13.	40.567	53.567	48.033	47.233	50.400	42.933	41.103	56.767	39.233	40.900	46.200	50.067	44.067	42.533	53.267
14.	43.000	34.600	51.033	42.500	45.133	44.067	37.900	39.667	44.167	42.667	47.700	51.967	45.400	47.433	49.917
15.	56.033	34.773	43.533	39.889	40.367	44.533	44.767	44.867	50.500	36.533	47.400	47.700	41.167	43.067	48.700

REPLICATION-2.

	18	29	44	59	74	89	104	119	134	149	164	179	194	209	224
1.	51.733	50.433	45.267	44.567	46.067	63.733	49.067	49.333	50.700	48.370	46.133	42.267	46.533	59.967	48.100
2.	41.533	49.100	49.741	48.400	43.733	53.000	54.300	51.067	56.433	44.100	44.333	66.333	39.967	42.467	45.741
3.	53.133	39.667	42.200	49.467	41.333	50.067	50.700	44.333	50.100	38.100	44.333	47.567	47.467	49.100	49.464
4.	51.233	50.889	50.433	38.867	50.067	30.889	43.533	40.300	47.867	47.367	39.700	38.000	49.833	45.967	45.967
5.	53.667	57.333	52.167	48.067	46.867	51.400	53.767	53.767	48.567	42.593	48.033	46.933	49.533	48.000	57.633
6.	49.467	38.233	37.900	58.167	48.733	46.067	43.200	37.400	48.133	44.433	50.267	48.733	31.333	50.467	42.667
7.	39.233	49.667	53.500	46.704	45.000	42.500	40.233	47.733	38.700	44.867	48.333	47.100	50.633	46.000	54.711
8.	47.433	43.500	37.667	53.300	43.593	48.267	54.200	49.067	55.233	52.567	46.667	48.167	41.300	44.500	44.367
9.	59.233	43.400	41.733	36.467	46.700	45.167	44.667	36.900	51.033	44.733	42.700	48.733	40.833	57.467	52.733
10.	33.533	47.500	40.667	44.733	44.267	45.800	42.867	48.167	36.833	51.067	43.167	41.000	47.667	51.667	47.167
11.	53.033	41.367	43.667	50.000	45.167	50.167	44.200	46.367	43.933	40.500	42.767	44.933	43.133	42.600	48.433
12.	49.767	49.667	34.567	47.167	45.667	50.867	43.633	48.433	50.733	56.370	44.333	44.833	45.367	44.967	43.133
13.	49.100	45.167	45.667	47.267	52.967	47.533	47.633	37.933	45.167	47.333	51.222	47.200	41.567	41.033	48.833
14.	48.900	46.733	50.600	41.259	40.056	41.933	41.367	48.200	59.367	44.926	49.900	42.267	41.533	56.000	46.833
15.	49.300	40.333	49.967	34.500	55.067	46.267	42.300	44.133	37.033	45.067	43.900	47.933	40.767	39.167	43.167

REPLICATION-3.

	45	59	73	97	101	115	129	143	157	171	195	199	213	2	16
1.	44.467	43.433	49.600	48.867	49.467	48.533	54.067	47.867	47.900	43.600	43.667	50.033	48.300	48.000	43.500
2.	42.200	50.400	43.200	51.967	53.933	55.233	48.933	42.267	58.133	54.033	44.967	45.733	49.800	44.367	60.333
3.	55.967	55.400	57.533	44.167	51.767	46.533	46.967	45.000	40.733	52.267	53.767	41.133	44.933	44.100	47.167
4.	47.100	54.433	46.500	47.167	43.766	44.133	50.400	46.342	48.533	44.200	48.522	49.567	52.633	44.000	41.700
5.	42.767	53.600	49.100	40.267	46.733	43.300	51.333	41.333	46.933	46.467	44.067	42.367	43.300	52.233	52.367
6.	51.500	42.033	45.367	46.233	47.233	45.033	49.133	39.033	53.967	49.200	44.967	46.700	49.700	50.133	45.133
7.	50.567	42.867	55.233	47.967	42.200	44.733	41.000	37.267	51.667	51.800	43.633	44.667	49.267	43.067	49.407
8.	50.867	47.733	42.533	50.167	50.967	42.833	49.033	48.233	50.567	41.200	47.900	45.567	41.933	42.400	52.033
9.	53.800	43.467	49.067	41.400	56.033	45.467	48.800	47.667	46.000	52.533	54.201	44.867	40.600	48.433	54.467
10.	43.967	39.733	44.233	44.267	44.200	47.267	43.467	45.233	48.900	48.167	43.267	45.033	50.933	45.333	56.100
11.	51.903	43.200	53.500	45.167	46.400	37.233	46.867	46.900	51.333	42.467	45.800	40.067	42.467	52.133	47.567
12.	51.867	46.900	51.533	44.700	44.633	50.167	56.600	43.500	43.100	43.700	33.867	41.800	43.300	41.833	41.067
13.	49.433	48.000	45.900	43.100	47.000	41.267	44.233	48.567	43.800	44.267	41.200	42.633	61.833	36.700	45.900
14.	51.233	46.167	39.867	51.200	51.967	43.733	55.467	49.433	43.733	48.333	43.133	49.633	44.767	47.900	49.800
15.	45.533	46.833	40.967	46.567	46.700	45.267	49.300	47.067	47.200	45.400	53.733	50.667	41.933	40.333	52.533

APPENDIX X Weight of seeds per spike at Ellerslie

233

ELLERSLIE REPLICATION-1. WEIGHT OF SEEDS PER SPIKE															
(Block)	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
1.	1.977	2.081	1.656	2.417	1.886	2.186	2.008	1.865	2.147	1.750	1.911	1.781	1.605	1.731	2.359
2.	1.596	2.043	1.775	1.755	1.825	2.113	2.268	1.864	1.958	1.940	2.320	1.515	1.711	2.051	1.500
3.	2.11	2.12	2.13	2.14	2.15	2.16	2.17	2.18	2.19	2.20	2.21	2.22	2.23	2.24	2.25
4.	2.044	1.666	1.850	1.868	2.092	2.022	2.051	1.789	1.964	2.018	1.493	2.098	1.745	1.570	1.748
5.	1.667	1.817	1.752	1.418	1.901	1.844	2.011	1.580	1.784	1.598	2.358	1.937	1.873	1.460	1.664
6.	1.776	1.256	1.705	1.686	1.897	1.868	2.126	1.654	1.513	1.966	1.559	1.819	1.750	1.800	1.601
7.	1.880	2.143	1.453	1.160	1.907	1.800	2.216	1.866	2.005	1.522	1.688	1.427	2.132	1.539	1.742
8.	2.247	1.983	1.867	1.812	1.990	2.344	1.332	1.619	1.898	1.729	1.998	1.912	1.818	1.022	1.632
9.	1.804	1.794	1.934	2.329	1.620	1.847	1.905	1.897	1.440	1.661	1.735	1.939	1.841	1.657	2.260
10.	1.753	1.697	1.561	1.533	1.468	1.785	1.511	1.618	1.877	1.561	1.954	1.997	1.365	1.561	1.879
11.	1.587	1.923	2.227	1.991	1.748	1.893	1.415	1.864	1.707	1.359	1.648	1.714	1.307	1.814	1.510
12.	1.417	1.401	1.750	1.615	1.522	1.474	1.569	1.749	1.980	1.524	1.794	1.494	1.555	1.629	1.339
13.	1.456	1.984	1.576	1.164	1.554	1.705	1.836	1.529	1.984	1.578	1.523	1.635	1.435	1.628	2.067
14.	1.607	1.813	1.976	1.813	1.887	1.727	1.606	2.265	1.629	1.465	1.854	1.925	1.513	1.741	1.878
15.	1.283	1.350	1.685	1.622	1.504	1.506	1.359	1.613	1.570	1.587	1.464	1.757	1.688	1.764	2.020
16.	1.953	1.325	1.689	1.559	1.492	1.681	1.973	1.973	1.602	1.371	1.507	1.692	1.467	1.604	1.673
REPLICATION-2.															
	14	29	44	59	74	89	104	119	134	149	164	179	194	209	224
1.	1.689	1.955	1.553	1.576	1.699	2.375	1.878	1.631	1.994	1.957	1.876	1.750	1.566	2.494	1.740
2.	1.637	1.886	1.685	1.680	1.695	1.924	2.301	1.796	2.172	1.870	2.133	2.331	1.679	1.625	1.735
3.	1.949	1.570	1.627	1.769	1.800	2.110	2.098	1.678	2.008	1.696	1.933	1.719	2.045	1.984	1.842
4.	1.872	2.139	2.099	1.625	1.629	1.193	1.692	1.378	1.727	1.754	1.459	1.485	1.885	1.540	1.616
5.	2.042	1.864	1.873	1.827	1.894	1.791	2.162	1.860	1.665	1.530	1.671	1.475	1.801	1.763	2.431
6.	2.103	1.513	1.547	2.128	1.674	1.611	1.853	1.420	1.887	1.698	1.709	1.560	1.204	2.048	1.394
7.	1.341	1.636	1.999	1.631	1.687	1.816	1.432	2.005	1.530	1.826	2.007	1.380	1.661	1.754	2.075
8.	2.001	1.785	1.473	1.839	1.646	1.878	1.852	1.812	2.190	1.984	1.524	1.899	1.721	1.822	1.759
9.	2.337	1.474	1.749	1.633	1.630	1.506	1.564	1.444	1.719	1.624	1.625	1.913	1.497	1.807	1.833
10.	1.487	1.572	1.385	1.540	1.589	1.515	1.443	1.900	1.475	1.656	1.431	1.658	1.575	1.825	1.792
11.	1.732	1.412	1.639	1.887	1.890	1.797	1.888	1.654	1.571	1.459	1.504	1.604	1.670	2.07	2.22
12.	1.855	1.622	1.205	1.594	1.779	1.606	1.603	2.275	1.799	2.061	1.556	1.548	1.561	1.701	1.469
13.	1.950	1.431	1.648	1.720	2.000	1.733	1.540	1.438	1.540	2.036	1.578	1.619	1.517	1.562	1.893
14.	1.518	1.682	1.913	1.625	1.208	1.511	1.618	1.856	2.016	1.704	1.564	1.701	1.755	1.922	1.783
15.	1.664	1.454	1.854	1.464	2.105	1.680	1.331	1.442	1.841	1.815	1.338	1.514	1.538	1.418	1.331
REPLICATION-3.															
	45	59	73	87	101	115	129	143	157	171	185	199	213	227	241
1.	1.688	1.515	1.925	1.755	2.279	1.966	1.792	1.740	1.795	1.519	1.620	2.268	1.918	1.780	1.656
2.	1.644	2.075	1.726	1.985	2.258	2.018	1.640	1.899	2.674	2.074	2.120	1.644	1.850	1.935	2.430
3.	2.267	2.267	2.653	1.599	2.389	2.102	1.752	2.069	1.991	2.260	2.504	1.493	1.986	1.609	1.656
4.	1.745	2.218	1.829	1.658	1.920	1.721	1.597	1.729	2.155	1.734	1.881	1.932	2.167	1.636	1.612
5.	1.369	2.006	1.738	1.613	1.755	1.583	1.859	1.605	1.812	1.963	1.725	1.524	1.842	1.750	1.583
6.	1.792	1.543	1.658	1.970	1.769	1.390	1.828	1.384	1.827	1.595	1.648	1.573	1.741	1.808	1.647
7.	1.575	1.520	2.263	1.869	1.522	1.569	1.561	1.551	2.013	2.010	1.506	1.581	1.931	1.724	1.756
8.	1.927	1.779	1.364	2.248	1.885	1.671	1.754	1.669	1.776	1.636	1.659	1.689	1.994	1.655	2.038
9.	2.112	1.639	1.876	1.659	2.182	1.733	1.747	1.757	1.492	1.734	0.487	1.695	1.405	2.013	2.143
10.	1.960	1.578	1.575	1.668	1.733	1.976	1.801	1.905	1.919	1.641	1.842	1.621	1.795	1.811	1.658
11.	2.039	1.686	1.882	1.623	1.686	1.182	1.813	1.851	2.066	1.977	1.494	1.333	2.026	2.084	1.717
12.	1.571	1.510	1.781	1.589	1.731	1.852	2.102	1.528	1.557	1.697	1.330	1.701	1.741	1.570	1.631
13.	1.827	1.769	1.616	1.838	1.400	1.464	1.391	1.766	1.802	1.580	1.583	1.561	2.008	1.344	1.608
14.	1.850	1.572	1.389	1.750	1.978	1.541	2.025	1.971	1.739	1.815	1.836	1.923	1.561	1.667	1.798
15.	1.663	1.836	1.420	1.458	1.818	1.443	1.655	1.998	1.516	1.612	2.043	1.946	1.614	1.529	1.944

APPENDIX XI 1000-kernel weight at Ellerslie

234

ELLERSLIE REPLICATION-1. 1000-KERNEL-WEIGHT															
(block)	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
1.	44.368	41.659	37.389	41.811	43.067	42.240	40.871	44.564	43.958	42.656	40.306	38.456	37.351	38.772	41.058
2.	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
3.	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225
4.	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
5.	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
6.	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135
7.	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
8.	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
9.	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165
10.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
11.	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210
12.	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
13.	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150
14.	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
15.	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180

REPLICATION-2.															
1.	14	29	44	59	74	89	104	119	134	149	164	179	194	209	224
2.	1	16	31	46	61	76	91	106	121	136	151	166	181	196	211
3.	9	24	39	54	69	84	99	114	129	144	159	174	189	204	219
4.	2	17	32	47	62	77	92	107	122	137	152	167	182	197	212
5.	6	21	36	51	66	81	96	111	126	141	155	171	186	201	216
6.	11	26	41	56	71	86	101	116	131	146	161	176	191	206	221
7.	16	31	46	61	76	91	106	121	136	151	166	181	196	211	226
8.	21	36	51	66	81	96	111	126	141	156	171	186	201	216	231
9.	26	41	56	71	86	101	116	131	146	161	176	191	206	221	236
10.	31	46	61	76	91	106	121	136	151	166	181	196	211	226	241
11.	36	51	66	81	96	111	126	141	156	171	186	201	216	231	246
12.	41	56	71	86	101	116	131	146	161	176	191	206	221	236	251
13.	46	61	76	91	106	121	136	151	166	181	196	211	226	241	256
14.	51	66	81	96	111	126	141	156	171	186	201	216	231	246	261
15.	56	71	86	101	116	131	146	161	176	191	206	221	236	251	266

REPLICATION-3.															
1.	45	59	73	87	101	115	129	143	157	171	185	199	213	2	16
2.	150	164	178	192	206	220	234	248	262	276	290	304	318	332	346
3.	90	104	118	132	146	160	174	188	202	216	230	244	258	272	286
4.	195	209	223	237	251	265	279	293	307	321	335	349	363	377	391
5.	105	119	133	147	161	175	189	203	217	231	245	259	273	287	301
6.	180	194	208	222	236	250	264	278	292	306	320	334	348	362	376
7.	60	74	88	102	116	130	144	158	172	186	200	214	228	242	256
8.	15	29	43	57	71	85	99	113	127	141	155	169	183	197	211
9.	225	239	253	267	281	295	309	323	337	351	365	379	393	407	421
10.	135	149	163	177	191	205	219	233	247	261	275	289	303	317	331
11.	165	179	193	207	221	235	249	263	277	291	305	319	333	347	361
12.	120	134	148	162	176	190	204	218	232	246	260	274	288	302	316
13.	30	44	58	72	86	100	114	128	142	156	170	184	198	212	226
14.	75	89	103	117	131	145	159	173	187	201	215	229	243	257	271
15.	210	224	238	252	266	280	294	308	322	336	350	364	378	392	406

APPENDIX XII Yield per plant at Ellerslie

235

ELLERSLIE REPLICATION-1. YIELD PER PLANT															
(Block)	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
1.	20.014	13.998	16.148	22.458	21.632	17.541	13.566	13.470	18.172	17.714	15.488	12.119	15.510	16.739	18.109
	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
2.	12.249	11.896	15.991	16.370	16.435	13.226	11.784	14.670	15.489	15.076	16.119	14.177	15.591	13.369	12.445
	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225
3.	12.612	13.550	15.513	13.904	16.101	16.135	14.991	12.710	15.474	15.691	12.365	13.568	14.305	14.986	11.921
	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
4.	13.727	16.053	17.340	13.761	17.710	15.785	14.996	10.474	13.311	10.408	14.041	10.739	16.172	10.910	14.602
	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
5.	14.839	8.817	15.195	11.829	14.388	15.894	20.396	20.287	13.004	16.658	15.056	16.841	10.994	17.030	13.992
	121	122	123	124	125	126	127	128	129	130	131	112	133	134	135
6.	19.515	15.609	12.524	10.622	16.662	12.891	15.938	14.263	19.275	15.397	15.926	15.112	19.708	12.103	17.097
	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
7.	21.035	17.076	15.016	16.612	16.779	18.588	13.965	20.560	17.213	18.243	14.550	16.880	20.034	13.873	14.405
	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
8.	13.359	16.750	13.478	16.782	11.726	12.923	14.522	20.174	13.217	18.664	11.659	12.418	13.996	14.083	17.843
	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165
9.	13.742	14.299	11.517	11.389	10.290	10.483	9.650	12.208	18.201	11.624	15.564	13.034	12.536	13.832	17.507
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
10.	13.674	11.962	12.898	16.687	13.607	12.430	10.620	12.986	0.0	9.050	13.767	12.562	12.660	13.845	12.816
	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210
11.	9.544	10.004	11.515	9.025	12.382	9.417	9.025	10.511	11.754	9.270	11.062	9.411	9.190	8.451	10.261
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
12.	10.185	13.110	11.849	7.109	12.268	13.613	10.706	11.114	18.510	11.058	12.664	12.443	11.909	13.118	12.534
	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150
13.	13.092	11.187	17.638	10.470	14.666	16.122	9.011	16.737	11.956	9.440	11.775	13.399	11.724	10.283	11.368
	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
14.	9.046	11.520	16.711	9.522	10.323	9.368	10.108	11.785	12.407	11.846	12.572	11.733	11.195	10.214	15.464
	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180
15.	13.802	8.938	14.956	9.301	10.016	12.397	15.049	17.030	11.062	10.918	11.432	13.473	11.245	11.289	10.557

REPLICATION-2.															
	14	29	44	59	74	89	104	119	134	149	164	179	194	209	224
1.	11.306	11.297	10.156	11.355	13.642	16.957	15.105	12.850	18.219	17.192	18.386	17.957	13.041	15.180	16.184
2.	12.560	14.333	15.252	13.631	15.949	16.779	16.139	12.732	16.860	12.982	16.826	15.725	13.976	15.629	19.521
3.	15.925	14.592	15.565	13.731	15.630	19.713	23.782	15.343	15.691	17.960	20.565	20.370	17.615	21.674	30.133
4.	17.239	14.089	13.860	13.495	14.506	11.108	16.985	11.575	11.536	13.539	15.021	12.338	14.641	17.139	16.236
5.	21.382	15.403	14.195	23.072	15.603	12.574	17.557	14.172	16.868	14.854	20.559	18.654	17.457	16.760	31.741
6.	19.914	12.657	18.268	17.355	18.684	16.184	17.616	13.181	14.605	13.760	16.580	12.701	10.053	14.354	16.760
7.	9.774	11.804	13.666	12.029	17.711	18.256	12.585	14.997	9.262	15.680	19.104	12.507	13.043	16.230	13.650
8.	19.907	21.396	14.271	14.755	22.785	14.840	15.605	14.739	22.907	14.874	14.289	13.060	14.801	15.934	20.220
9.	16.650	13.324	16.846	15.777	17.734	15.994	14.243	13.795	16.188	15.238	15.529	20.041	16.782	12.477	15.692
10.	13.907	14.000	15.648	11.949	12.876	14.635	11.325	13.269	15.843	15.671	21.504	17.150	14.097	18.031	22.695
11.	17.950	10.206	19.312	15.778	11.894	14.868	16.663	14.462	13.845	14.348	17.113	14.922	17.194	19.268	16.447
12.	13.275	18.256	13.490	12.960	16.980	15.652	23.694	25.419	17.875	23.379	12.881	16.522	19.064	19.127	17.974
13.	14.721	10.751	18.560	16.719	14.615	12.534	19.344	8.611	9.223	13.028	10.780	10.284	13.500	14.484	15.423
14.	11.835	12.733	13.089	15.454	11.717	14.165	15.347	19.603	18.548	13.158	15.482	20.703	13.155	13.746	13.595
15.	13.354	12.145	11.736	13.029	15.353	19.624	10.181	11.180	13.989	14.564	15.053	14.182	14.526	19.322	20.700

REPLICATION-3.															
	45	59	73	87	101	115	129	143	157	171	185	199	213	2	16
1.	17.441	17.404	16.490	17.434	22.527	24.381	20.277	18.339	15.906	21.744	18.427	17.252	20.047	22.004	15.460
2.	24.942	21.535	15.136	21.058	20.569	17.690	18.116	20.850	19.031	19.355	19.118	22.259	12.833	19.449	14.787
3.	20.586	21.503	17.903	28.528	19.283	13.324	16.519	17.330	17.268	16.586	18.945	14.152	17.809	16.345	14.238
4.	22.096	22.987	16.527	14.920	17.038	20.476	14.965	19.187	16.570	23.909	17.817	17.203	21.004	22.804	26.440
5.	13.308	17.902	22.006	20.777	21.962	19.065	21.014	16.658	18.189	19.445	14.177	20.918	16.189	20.555	14.343
6.	15.170	13.263	23.873	17.493	18.198	23.213	14.884	18.114	13.013	14.689	14.671	18.246	12.202	13.274	15.043
7.	16.055	14.390	17.700	14.414	11.251	13.973	18.037	16.397	23.367	15.253	15.644	16.257	23.399	19.945	13.347
8.	29.280	19.804	20.872	17.375	19.031	17.918	23.879	28.027	19.399	14.238	16.754	16.429	17.771	12.233	15.733
9.	14.915	21.034	21.933	16.076	24.041	18.957	19.013	16.347	13.328	22.301	18.315	17.703	13.965	24.916	20.776
10.	18.209	15.468	15.947	20.888	18.007	19.287	19.274	15.306	18.549	22.011	20.388	16.864	21.393	16.303	15.758
11.	18.436	15.198	15.443	15.387	17.445	21.102	26.331	19.778	14.034	28.225	21.637	20.184	17.927	16.782	24.445
12.	11.361	19.413	13.832	17.081	15.816	14.150	15.748	15.137	14.785	14.995	10.151	14.700	15.734	20.912	20.908
13.	13.239	13.191	15.769	17.734	13.016	13.264	16.735	14.196	19.209	11.270	13.764	18.630	12.940	17.481	13.268
14.	14.445	20.732	14.236	14.660	15.843	15.603	16.201	16.491	13.107	14.622	18.040	17.002	15.124	10.136	17.724
15.	210	224	13	27	41	55	69	83	97	111	125	139	153	167	181
15.	9.688	15.049	9.347	15.678	20.549	15.720	18.553	14.946	10.728	13.063	16.554	14.268	15.512	19.198	28.554

APPENDIX XIII Onset-of-heading at Parkland

PARKLAND REPLICATION-1

(Block)	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
1.	46.000	48.000	54.000	52.000	49.000	49.000	49.000	49.000	52.000	49.000	48.000	49.000	51.000	51.000	49.000
	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
2.	48.000	48.000	51.000	48.000	51.000	51.000	44.000	44.000	46.000	50.000	47.000	51.000	54.000	50.000	52.000
	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225
3.	50.000	48.000	55.000	45.000	48.000	48.000	50.000	48.000	46.000	52.000	48.000	48.000	53.000	54.000	52.000
	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
4.	52.000	48.000	48.000	52.000	48.000	46.000	49.000	51.000	52.000	48.000	50.000	48.000	49.000	56.000	57.000
	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
5.	50.000	55.000	50.000	50.000	57.000	55.000	54.000	52.000	55.000	49.000	52.000	53.000	51.000	48.000	52.000
	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135
6.	52.000	52.000	53.000	51.000	49.000	52.000	53.000	49.000	49.000	52.000	51.000	49.000	48.000	51.000	49.000
	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
7.	53.000	53.000	57.000	53.000	49.000	53.000	57.000	57.000	50.000	50.000	48.000	55.000	52.000	49.000	53.000
	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
8.	57.000	57.000	52.000	48.000	50.000	46.000	55.000	48.000	49.000	46.000	54.000	50.000	56.000	49.000	52.000
	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165
9.	48.000	52.000	49.000	52.000	55.000	52.000	57.000	55.000	48.000	48.000	55.000	52.000	53.000	53.000	50.000
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
10.	53.000	50.000	49.000	52.000	48.000	49.000	58.000	48.000	58.000	53.000	45.000	53.000	52.000	58.000	49.000
	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210
11.	53.000	54.000	55.000	52.000	53.000	51.000	52.000	49.000	49.000	54.000	52.000	54.000	52.000	52.000	54.000
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
12.	50.000	49.000	50.000	55.000	48.000	54.000	53.000	52.000	52.000	56.000	50.000	48.000	53.000	49.000	54.000
	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150
13.	49.000	58.000	53.000	52.000	140	141	142	143	144	145	146	147	148	149	150
	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
14.	57.000	53.000	58.000	51.000	58.000	55.000	54.000	49.000	54.000	55.000	57.000	52.000	53.000	56.000	53.000
	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180
15.	56.000	53.000	55.000	55.000	54.000	56.000	53.000	53.000	58.000	53.000	57.000	53.000	54.000	52.000	54.000

REPLICATION-2

	13	29	44	59	74	99	104	119	134	149	164	179	194	209	224
1.	68.000	56.000	57.000	60.000	60.000	58.000	58.000	57.000	57.000	56.000	57.000	57.000	58.000	56.000	57.000
	1	16	31	46	61	76	91	106	121	136	151	166	181	196	211
2.	57.000	59.000	57.000	57.000	57.000	57.000	58.000	60.000	57.000	59.000	58.000	60.000	56.000	57.000	60.000
	9	24	39	54	69	84	99	114	129	144	159	174	189	204	219
3.	68.000	57.000	57.000	61.000	56.000	57.000	58.000	64.000	58.000	56.000	62.000	54.000	57.000	56.000	56.000
	2	17	32	47	62	77	92	107	122	137	152	167	182	197	212
4.	58.000	56.000	55.000	55.000	60.000	57.000	57.000	70.000	58.000	59.000	57.000	57.000	56.000	58.000	64.000
	6	21	36	51	66	81	96	111	126	141	156	171	186	201	216
5.	56.000	60.000	59.000	57.000	57.000	53.000	57.000	59.000	58.000	57.000	59.000	59.000	57.000	57.000	57.000
	11	26	41	56	71	86	101	116	131	146	161	176	191	206	221
6.	57.000	57.000	56.000	57.000	58.000	64.000	56.000	59.000	58.400	59.000	60.000	71.000	58.000	57.000	57.000
	10	25	40	55	70	85	100	115	130	145	160	175	190	205	220
7.	58.000	57.000	60.000	57.000	58.000	60.000	65.000	56.000	60.000	58.000	56.000	56.000	56.000	57.000	57.000
	8	23	38	53	68	83	98	113	128	143	158	173	188	203	218
8.	56.000	56.000	57.000	56.000	56.000	56.000	57.000	57.000	56.000	58.000	69.000	56.000	56.000	56.000	58.000
	3	18	33	48	63	78	93	108	123	138	153	168	183	198	213
9.	56.000	59.000	56.000	57.000	58.000	64.000	59.000	56.000	59.000	56.000	57.000	57.000	56.000	60.000	58.000
	13	28	43	58	73	88	103	118	133	148	163	178	193	208	223
10.	59.000	58.000	57.000	58.000	59.000	57.000	53.000	58.000	56.000	59.000	58.000	57.000	57.000	56.000	53.000
	12	27	42	57	72	87	102	117	132	147	162	177	192	207	222
11.	61.000	57.000	56.000	57.000	56.000	57.000	58.000	58.000	58.000	57.000	57.000	55.000	58.000	59.000	56.000
	5	20	35	50	65	80	95	110	125	140	155	170	185	200	215
12.	57.000	58.000	56.000	58.000	57.000	63.000	57.000	61.000	57.000	57.000	58.000	56.000	56.000	57.000	56.000
	4	19	34	49	64	79	94	109	124	139	154	169	184	199	214
13.	58.000	58.000	59.000	59.000	57.000	58.000	57.000	62.000	59.000	57.000	60.000	58.000	58.000	57.000	57.000
	7	22	37	52	67	82	97	112	127	142	157	172	187	202	217
14.	69.000	57.000	58.000	56.000	59.000	59.000	59.000	59.000	58.000	56.000	60.000	57.000	57.000	58.000	60.000
	15	30	45	60	75	90	105	120	135	150	165	180	195	210	225
15.	59.000	60.000	58.000	70.000	58.000	58.000	60.000	59.000	59.000	58.000	57.000	59.000	59.000	58.000	57.000

REPLICATION-3.															
	85	99	73	87	101	115	129	143	157	171	185	199	213	2	16
1.	56.000	58.000	52.000	49.000	49.000	50.000	53.000	54.000	48.000	48.000	48.000	49.000	50.000	48.000	52.000
	150	164	178	192	206	220	9	23	37	51	65	79	93	107	121
2.	52.000	57.000	53.000	49.000	50.000	53.000	57.000	52.000	52.000	53.000	52.000	50.000	58.000	57.000	54.000
	90	104	118	132	146	160	174	188	202	216	5	19	33	47	61
3.	50.000	48.000	48.000	50.000	48.000	47.000	51.000	47.000	50.000	49.000	49.000	50.000	48.000	47.000	53.000
	195	209	223	12	26	40	54	68	82	96	110	124	138	152	166
4.	50.000	47.000	54.000	57.000	48.000	56.000	54.000	48.000	56.000	57.000	55.000	53.000	47.000	54.000	53.000
	105	119	133	147	161	175	189	203	217	6	20	34	48	62	76
5.	54.000	52.000	48.000	48.000	54.000	48.000	53.000	50.000	53.000	48.000	54.000	53.000	51.000	58.000	58.000
	180	194	208	222	11	25	39	53	67	81	95	109	123	137	151
6.	52.000	53.000	49.000	47.000	46.000	52.000	52.000	55.000	55.000	54.000	51.000	53.000	55.000	58.000	49.000
	60	74	88	102	116	130	144	158	172	186	200	214	3	17	31
7.	58.000	53.000	50.000	52.000	52.000	54.000	49.000	58.000	52.000	52.000	52.000	49.000	50.000	47.000	50.000
	15	29	43	57	71	85	99	113	127	141	155	169	183	197	211
8.	47.000	48.000	50.000	48.000	54.000	50.000	52.000	49.000	55.000	53.000	55.000	54.000	47.000	53.000	50.000
	225	14	28	42	56	70	84	98	112	126	140	154	168	182	196
9.	52.000	58.000	53.000	46.000	50.000	47.000	52.000	53.000	53.000	53.000	48.000	49.000	52.000	48.000	50.000
	135	149	163	177	191	205	219	8	22	36	50	64	78	92	106
10.	46.000	46.000	53.000	52.000	48.000	50.000	48.000	48.000	50.000	50.000	48.000	52.000	55.000	48.000	53.000
	165	179	193	207	221	10	24	38	52	66	80	94	108	122	136
11.	52.000	49.000	53.000	53.000	47.000	53.000	48.000	53.000	46.000	48.000	58.000	49.000	48.000	53.000	48.000
	120	134	148	162	176	190	204	218	7	21	35	49	63	77	91
12.	50.000	53.000	57.000	49.000	55.000	50.000	49.000	48.000	57.000	53.000	49.000	53.000	48.000	48.000	50.000
	30	44	58	72	86	100	114	128	142	156	170	184	198	212	1
13.	50.000	52.000	49.000	52.000	54.000	52.000	54.000	52.000	48.000	53.000	52.000	53.000	55.000	55.000	53.000
	75	89	103	117	131	145	159	173	187	201	215	4	18	32	46
14.	52.000	50.000	48.000	49.000	50.000	51.000	52.000	49.000	52.000	48.000	48.000	47.000	53.000	49.000	53.000
	210	224	13	27	41	55	69	83	97	111	125	139	153	167	181
15.	52.000	56.000	48.000	53.000	48.000	50.000	49.000	48.000	58.000	48.000	52.000	50.000	47.000	48.000	48.000

PARKLAND		REPLICATION-1													
(Block)	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
1.	57.000	56.000	59.000	57.000	57.000	59.000	59.000	58.000	57.000	60.000	58.000	59.000	59.000	60.000	59.000
2.	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
3.	59.000	57.000	61.000	56.000	58.000	57.000	60.000	59.000	52.000	60.000	59.000	57.000	59.000	60.000	57.000
4.	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
5.	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
6.	58.000	58.000	57.000	59.000	57.000	59.000	58.000	56.000	58.000	59.000	59.000	59.000	57.000	57.000	56.000
7.	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
8.	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
9.	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165
10.	59.000	58.000	56.000	57.000	56.000	56.000	60.000	57.000	62.000	61.000	56.000	60.000	58.000	60.000	57.000
11.	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210
12.	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
13.	59.000	57.000	56.000	60.000	58.000	59.000	58.000	58.000	59.000	60.000	56.000	56.000	59.000	57.000	59.000
14.	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150
15.	59.000	60.000	57.000	58.000	60.000	59.000	58.000	59.000	57.000	58.000	59.000	59.000	58.000	61.000	59.000

REPLICATION-2															
1.	14	29	44	59	74	89	104	119	134	149	164	179	194	209	224
2.	1	16	31	46	61	76	91	106	121	136	151	166	181	196	211
3.	9	24	39	54	69	84	99	114	129	144	159	174	189	204	219
4.	2	17	32	47	62	77	92	107	122	137	152	167	182	197	212
5.	6	21	36	51	66	81	96	111	126	141	156	171	186	201	216
6.	11	26	41	56	71	86	101	116	131	146	161	176	191	206	221
7.	10	25	40	55	70	85	100	115	130	145	160	175	190	205	220
8.	8	23	38	53	68	83	98	113	128	143	158	173	188	203	218
9.	3	18	33	48	63	78	93	108	123	138	153	168	183	198	213
10.	13	28	43	58	73	88	103	118	133	148	163	178	193	208	223
11.	12	27	42	57	72	87	102	117	132	147	162	177	192	207	222
12.	5	20	35	50	65	80	95	110	125	140	155	170	185	200	215
13.	8	19	34	49	64	79	94	109	124	139	154	169	184	199	214
14.	7	22	37	52	67	82	97	112	127	142	157	172	187	202	217
15.	15	30	45	60	75	90	105	120	135	150	165	180	195	210	225

REPLICATION-3															
1.	45	59	73	87	101	115	129	143	157	171	185	199	213	2	16
2.	150	164	178	192	206	220	9	23	37	51	65	79	93	107	121
3.	90	104	118	132	146	160	174	188	202	216	5	19	33	47	61
4.	195	209	223	12	26	40	54	68	82	96	110	124	138	152	166
5.	105	119	133	147	161	175	189	203	217	6	20	34	48	62	76
6.	180	194	208	222	11	25	39	53	67	81	95	109	123	137	151
7.	60	74	88	102	116	130	144	158	172	186	200	214	3	17	31
8.	15	29	43	57	71	85	99	113	127	141	155	169	183	197	211
9.	225	14	28	42	56	70	84	98	112	126	140	154	168	182	196
10.	135	149	163	177	191	205	219	8	22	36	50	64	78	92	106
11.	165	179	193	207	221	10	24	38	52	66	80	94	108	122	136
12.	120	134	148	162	176	190	204	218	7	21	35	49	63	77	91
13.	30	44	58	72	86	100	114	128	142	156	170	184	198	212	1
14.	75	89	103	117	131	145	159	173	187	201	215	4	18	32	46
15.	210	224	13	27	41	55	69	83	97	111	125	139	153	167	181

(Block)	PARTIAL REPLICATION-1														
	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
1.	11.000	8.000	5.000	5.000	8.000	9.000	10.000	9.000	5.000	11.000	10.000	11.000	5.000	7.000	9.000
2.	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
3.	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225
4.	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
5.	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
6.	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135
7.	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
8.	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
9.	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165
10.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
11.	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210
12.	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
13.	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150
14.	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
15.	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180

REPLICATION-2															
	14	29	44	59	74	89	104	119	134	149	164	179	194	209	224
1.	10.000	7.000	9.000	5.000	12.000	6.000	8.000	5.000	9.000	7.000	4.000	9.000	4.000	7.000	4.000
2.	6.000	5.000	8.000	4.000	8.000	7.000	6.000	3.000	7.000	5.000	10.000	5.000	7.000	9.000	9.000
3.	11.000	9.000	5.000	4.000	8.000	7.000	7.000	9.000	10.000	8.000	5.000	10.000	7.000	9.000	7.000
4.	9.000	8.000	7.000	3.000	5.000	9.000	5.000	13.000	5.000	4.000	4.000	9.000	7.000	5.000	9.000
5.	9.000	6.000	6.000	8.000	10.000	6.000	5.000	5.000	5.000	4.000	6.000	5.000	5.000	5.000	7.000
6.	5.000	9.000	10.000	4.000	5.000	9.000	8.000	7.000	6.000	8.000	5.000	13.000	11.000	4.000	4.000
7.	6.000	5.000	6.000	8.000	8.000	8.000	9.000	7.000	10.000	6.000	9.000	8.000	6.000	5.000	4.000
8.	6.000	8.000	7.000	5.000	7.000	7.000	4.000	7.000	6.000	6.000	11.000	7.000	8.000	8.000	10.000
9.	7.000	7.000	10.000	11.000	8.000	7.000	6.000	7.000	4.000	8.000	9.000	6.000	8.000	5.000	7.000
10.	4.000	4.000	8.000	10.000	8.000	7.000	9.000	8.000	8.000	6.000	9.000	4.000	4.000	7.000	4.000
11.	7.000	5.000	7.000	9.000	6.000	9.000	6.000	9.000	6.000	9.000	5.000	3.000	6.000	7.000	7.000
12.	9.000	6.000	6.000	6.000	5.000	5.000	6.000	7.000	7.000	7.000	3.000	7.000	8.000	9.000	7.000
13.	5.000	5.000	6.000	5.000	8.000	9.000	8.000	9.000	7.000	5.000	6.000	6.000	4.000	8.000	9.000
14.	11.000	8.000	7.000	8.000	7.000	3.000	11.000	10.000	5.000	8.000	5.000	9.000	8.000	6.000	6.000
15.	10.000	4.000	6.000	12.000	10.000	6.000	6.000	7.000	11.000	6.000	6.000	6.000	9.000	5.000	5.000

REPLICATION-3															
	45	59	73	87	101	115	129	143	157	171	185	199	213	2	16
1.	2.000	3.000	5.000	6.000	5.000	5.000	5.000	4.000	9.000	8.000	9.000	7.000	7.000	8.000	5.000
	150	164	178	192	206	220	9	23	37	51	65	79	93	107	121
2.	6.000	6.000	6.000	7.000	4.000	5.000	8.000	4.000	5.000	5.000	6.000	5.000	7.000	6.000	4.000
	90	104	118	132	146	160	174	188	202	216	5	19	33	47	61
3.	5.000	6.000	6.000	5.000	6.000	4.000	6.000	4.000	4.000	5.000	4.000	5.000	5.000	5.000	5.000
	195	209	223	12	26	40	54	68	82	96	110	124	138	152	166
4.	5.000	5.000	5.000	4.000	5.000	5.000	5.000	4.000	5.000	6.000	7.000	6.000	5.000	6.000	6.000
	105	119	133	147	161	175	189	203	217	6	20	34	48	62	76
5.	5.000	7.000	5.000	5.000	6.000	6.000	5.000	6.000	5.000	4.000	6.000	5.000	6.000	6.000	7.000
	180	194	208	222	11	25	39	53	67	81	95	109	123	137	151
6.	7.000	7.000	6.000	6.000	5.000	5.000	5.000	5.000	4.000	7.000	6.000	7.000	6.000	8.000	6.000
	60	74	88	102	116	130	144	158	172	186	200	214	3	17	31
7.	7.000	7.000	5.000	5.000	6.000	6.000	7.000	7.000	5.000	5.000	6.000	5.000	5.000	5.000	6.000
	15	29	43	57	71	85	99	113	127	141	155	169	183	197	211
8.	6.000	5.000	7.000	5.000	7.000	5.000	6.000	6.000	5.000	6.000	7.000	4.000	6.000	6.000	10.000
	225	14	28	42	56	70	84	98	112	126	140	154	168	182	196
9.	6.000	7.000	5.000	5.000	6.000	6.000	7.000	6.000	5.000	7.000	5.000	6.000	7.000	5.000	9.000
	135	149	163	177	191	205	219	8	22	36	50	64	78	92	106
10.	5.000	6.000	5.000	7.000	8.000	6.000	5.000	5.000	4.000	6.000	5.000	6.000	0.000	6.000	6.000
	165	179	193	207	221	10	24	38	52	66	80	94	108	122	136
11.	7.000	5.000	5.000	5.000	6.000	5.000	5.000	5.000	4.000	5.000	8.000	6.000	5.000	6.000	6.000
	120	134	148	162	176	190	204	218	7	21	35	49	63	77	91
12.	6.000	5.000	7.000	5.000	7.000	6.000	6.000	6.000	7.000	6.000	6.000	5.000	5.000	6.000	4.000
	30	44	58	72	86	100	114	128	142	156	170	184	198	212	1
13.	5.000	6.000	6.000	6.000	8.000	5.000	7.000	6.000	5.000	5.000	6.000	7.000	5.000	7.000	6.000
	75	89	103	117	131	145	159	173	187	201	215	4	18	32	46
14.	6.000	5.000	8.000	6.000	6.000	5.000	6.000	4.000	5.000	5.000	6.000	6.000	7.000	5.000	6.000
	210	224	13	27	41	55	69	83	97	111	125	139	153	167	181
15.	7.000	4.000	5.000	7.000	5.000	6.000	5.000	5.000	7.000	6.000	6.000	6.000	6.000	7.000	6.000

PARKLAND		REPLICATION-1.										PLANT HEIGHT				
(Block)	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	
1.	71.950	73.550	108.760	90.300	93.440	83.850	95.440	74.550	99.440	76.450	75.960	95.010	98.870	101.520	102.610	
2.	71.040	75.250	105.610	53.270	111.550	115.330	79.240	83.810	76.510	109.440	73.520	115.070	115.100	80.840	107.240	
3.	91.150	94.680	90.700	74.970	76.900	94.230	101.300	77.030	76.030	104.580	106.120	74.540	98.710	85.550	91.220	
4.	102.570	78.440	87.710	118.470	85.930	107.370	81.460	102.330	118.070	106.370	105.980	77.480	104.360	123.940	113.410	
5.	104.360	120.150	77.140	104.210	127.330	126.400	109.370	94.860	121.360	78.870	103.910	115.400	80.850	88.850	98.680	
6.	106.800	93.410	122.270	92.690	91.770	109.620	122.260	82.760	95.700	97.230	96.210	89.770	76.170	97.720	71.590	
7.	76.000	82.240	120.840	110.520	84.540	78.440	120.880	112.340	102.620	93.470	76.960	78.400	78.820	94.250	104.330	
8.	99.190	120.790	101.260	93.010	87.650	75.750	117.890	82.940	83.260	107.880	115.710	79.640	117.070	84.270	88.070	
9.	75.110	112.010	105.660	125.140	123.480	109.730	127.500	129.460	76.890	81.180	105.720	104.880	94.480	76.060	90.230	
10.	103.190	79.230	77.300	105.240	74.490	69.910	126.930	76.380	125.160	81.960	73.290	102.310	97.340	126.790	87.670	
11.	97.760	99.260	116.800	75.990	103.830	95.970	82.090	80.460	85.520	108.020	95.340	106.070	97.350	76.350	105.640	
12.	78.500	79.360	80.270	103.760	95.330	113.990	90.230	98.620	80.720	116.110	80.100	76.090	98.410	91.470	99.670	
13.	81.850	124.640	76.480	75.660	109.620	110.990	79.830	109.800	82.230	109.560	77.790	78.450	123.830	82.430	99.080	
14.	124.600	96.210	126.240	93.440	131.290	111.030	87.050	81.260	108.490	107.820	126.020	102.270	84.660	96.460	79.830	
15.	110.150	80.920	105.660	104.000	115.240	99.900	78.550	80.200	123.760	94.770	130.110	94.220	109.430	80.140	103.220	

REPLICATION-2.		REPLICATION-2.										PLANT HEIGHT				
(Block)	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	
1.	112.670	67.080	91.160	120.350	72.570	89.610	85.390	83.480	89.430	70.140	70.240	68.440	98.140	72.510	76.160	
2.	95.270	73.900	79.020	101.290	98.050	94.490	98.630	117.100	70.320	95.450	69.860	104.760	67.030	71.310	104.490	
3.	117.380	76.580	75.580	101.590	78.250	102.960	103.460	118.760	101.210	80.730	74.440	116.440	94.370	77.840	74.160	
4.	78.340	74.820	75.330	78.550	115.510	91.290	82.490	125.910	95.620	118.800	104.020	74.060	70.100	94.970	99.060	
5.	75.090	115.390	102.580	109.090	75.650	106.390	75.830	114.940	102.270	98.410	116.280	83.860	76.160	83.590	90.570	
6.	77.060	75.840	79.620	98.320	110.060	118.270	80.230	94.560	92.000	80.160	110.530	123.530	100.880	91.420	91.500	
7.	77.990	100.950	112.180	95.970	103.050	100.080	90.370	74.500	85.440	102.220	72.230	92.020	73.200	100.810	95.260	
8.	70.440	91.900	93.520	102.750	77.790	78.270	109.810	87.340	76.420	94.790	121.340	79.040	75.330	77.040	72.730	
9.	74.830	106.170	78.030	81.650	101.130	117.990	117.630	75.240	118.220	83.790	93.730	101.380	93.900	115.650	95.730	
10.	83.533	113.811	108.980	107.150	119.600	100.840	78.440	75.530	82.010	123.730	84.920	108.710	100.790	116.590	99.700	
11.	112.870	116.680	75.360	77.130	74.890	94.370	77.300	97.540	77.630	77.540	94.080	78.750	100.280	84.830	68.310	
12.	64.680	100.330	89.520	92.540	90.170	124.420	86.460	123.900	86.570	105.950	119.750	99.660	95.910	94.070	80.590	
13.	100.230	92.420	106.530	106.320	96.400	89.730	99.080	114.516	92.760	77.490	119.760	102.550	87.640	74.170	75.170	
14.	120.650	80.010	90.060	78.910	124.730	91.720	127.260	111.660	119.470	75.920	119.950	73.790	83.640	77.230	104.350	
15.	100.260	111.360	96.780	126.700	103.000	84.300	113.850	83.330	86.570	99.150	87.500	105.740	105.740	106.120	98.800	

REPLICATION-3.		REPLICATION-3.										PLANT HEIGHT				
(Block)	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	
1.	90.060	109.040	103.670	79.060	70.590	73.570	94.010	118.680	90.740	90.430	100.335	77.800	105.420	79.260	74.340	
2.	95.460	70.520	107.300	95.420	92.170	105.840	118.730	80.410	75.420	90.780	94.300	87.840	109.940	107.420	95.840	
3.	79.870	93.880	76.130	80.180	76.880	75.210	112.200	75.970	79.120	92.560	77.490	95.520	74.560	73.560	90.950	
4.	79.020	77.840	101.930	112.910	75.600	114.520	111.750	73.570	86.530	81.100	121.890	89.430	76.390	114.760	106.680	
5.	108.700	86.700	79.540	82.310	110.880	87.430	100.670	80.280	113.760	74.920	108.280	102.930	76.180	114.010	114.920	
6.	100.560	109.650	114.720	77.260	81.150	99.830	80.330	107.580	114.210	101.580	84.950	99.800	119.430	118.430	70.600	
7.	116.360	80.600	98.160	73.850	87.190	90.680	76.940	124.710	90.210	81.380	97.420	81.090	74.510	76.660	85.820	
8.	86.940	70.280	102.480	84.520	113.770	107.420	96.440	97.760	114.910	102.040	119.560	104.340	98.350	107.040	90.780	
9.	95.600	123.540	117.680	75.270	103.920	106.820	109.670	116.470	109.900	113.380	103.550	90.620	101.100	79.670	83.780	
10.	78.980	74.710	90.290	96.530	100.310	101.730	79.520	75.070	78.680	105.240	79.890	97.570	119.840	81.700	104.640	
11.	81.430	76.360	103.140	96.240	90.860	87.910	81.540	111.680	86.690	76.110	116.240	105.140	77.600	102.860	77.480	
12.	83.480	101.540	122.620	106.880	122.600	80.780	80.540	79.180	121.690	115.340	98.700	109.660	99.480	101.750	74.720	
13.	88.910	109.160	114.640	77.670	120.000	88.100	119.740	84.740	82.000	117.220	91.750	90.100	118.290	108.590	101.230	
14.	65.520	84.500	87.490	100.110	92.470	106.960	79.840	81.300	96.780	90.670	82.290	104.240	114.720	76.390	97.830	
15.	100.540	108.580	81.110	118.030	81.000	108.830	87.190	83.470	125.340	113.120	95.270	76.530	91.330	80.390	76.120	

APPENDIX XVII Number of tillers per plant at Parkland

240

PARKLAND REPLICATION-1, NUMBER OF TILLERS PER PLANT															
(Block)	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
1.	15.400	12.000	13.200	12.800	16.000	11.600	12.200	12.600	11.300	12.700	11.900	13.700	12.300	15.200	11.000
2.	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
3.	12.900	12.800	14.500	12.100	13.500	16.200	12.500	12.800	11.800	13.700	11.300	14.800	14.100	13.200	12.500
4.	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225
5.	12.500	14.600	14.300	12.500	13.600	13.300	12.000	12.700	13.600	15.900	12.600	8.900	16.300	13.200	13.300
6.	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
7.	12.600	11.500	12.000	13.800	16.600	14.600	12.600	15.700	12.200	13.400	12.100	12.200	12.900	15.700	14.300
8.	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
9.	15.667	13.100	13.600	12.900	13.200	15.600	10.900	13.500	16.400	11.300	12.800	15.200	12.100	11.300	17.200
10.	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135
11.	15.400	12.400	12.600	14.000	10.400	12.400	13.700	11.000	11.200	12.100	14.200	14.900	12.000	10.600	12.700
12.	81	92	93	94	95	96	97	98	99	100	101	102	103	104	105
13.	10.200	13.100	14.100	12.200	8.200	10.500	16.800	11.100	14.200	13.000	11.300	12.800	10.800	13.800	11.500
14.	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
15.	15.100	14.200	13.300	10.700	11.600	14.400	13.700	11.000	14.300	12.400	14.000	10.100	14.400	14.700	11.800
16.	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165
17.	11.700	16.100	12.900	12.700	13.200	11.600	14.600	12.100	11.500	10.400	11.900	11.800	12.700	10.100	12.800
18.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
19.	15.300	17.100	10.400	13.800	11.900	11.700	13.300	10.300	13.400	13.100	11.400	11.300	14.100	12.900	17.600
20.	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210
21.	17.100	14.000	13.100	11.100	13.500	12.400	15.400	12.900	13.500	13.400	13.400	13.500	16.400	14.200	18.700
22.	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
23.	18.500	12.100	15.700	14.200	15.300	16.200	11.400	11.300	11.300	12.600	14.400	11.100	15.300	15.600	13.800
24.	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150
25.	16.300	15.700	13.000	10.400	12.500	16.300	11.300	13.900	12.400	13.800	12.400	12.500	13.500	19.800	12.700
26.	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
27.	18.800	11.000	14.400	12.800	13.200	12.600	13.500	13.600	11.900	15.300	14.500	11.400	12.000	15.300	15.000
28.	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180
29.	12.700	13.300	13.400	15.400	16.400	15.200	11.400	12.500	13.600	12.200	13.600	13.700	16.200	10.656	16.800

REPLICATION-2,

	12	29	44	59	74	89	104	119	134	149	164	179	194	209	224
1.	13.700	9.000	14.100	15.500	10.600	11.700	13.400	11.200	15.300	9.900	11.600	8.200	12.400	8.200	11.300
2.	1	16	31	46	61	76	91	106	121	136	151	166	181	196	211
3.	15.300	11.100	12.600	10.200	12.400	11.600	11.200	13.500	9.000	12.900	10.700	12.200	9.600	10.300	13.400
4.	9	24	39	54	69	84	99	114	129	144	159	174	189	204	219
5.	15.800	15.100	13.000	14.600	11.600	10.800	12.400	13.500	12.000	11.700	10.800	15.200	10.100	13.500	17.100
6.	2	17	32	47	62	77	92	107	122	137	152	167	182	197	212
7.	15.700	10.900	11.400	10.600	14.400	12.200	12.600	17.000	11.200	12.667	12.100	12.000	8.000	13.900	13.200
8.	6	21	36	51	66	81	96	111	126	141	156	171	186	201	216
9.	11.500	12.900	10.200	10.000	10.700	12.900	8.500	14.500	12.700	12.300	14.900	10.300	9.700	12.800	12.556
10.	11	26	41	56	71	86	101	116	131	146	161	176	191	206	221
11.	9.400	13.200	16.500	12.400	13.400	13.700	11.700	15.900	13.300	11.800	14.200	13.200	11.800	13.500	11.800
12.	10	25	40	55	70	85	100	115	130	145	160	175	190	205	220
13.	11.600	11.800	9.700	12.600	14.500	11.800	11.900	9.500	14.300	12.800	8.500	11.800	11.700	3.300	10.200
14.	8	23	38	53	68	83	98	113	128	143	158	173	188	203	218
15.	11.400	14.200	9.100	9.900	11.200	9.400	11.100	9.500	9.600	12.500	12.500	11.700	11.300	10.000	12.800
16.	3	18	33	48	63	78	93	108	123	138	153	168	183	198	213
17.	9.100	11.300	10.300	12.600	10.900	10.300	10.444	11.400	13.300	9.000	9.800	11.000	9.500	11.200	15.800
18.	13	28	43	58	73	88	103	118	133	148	163	178	193	208	223
19.	22.667	23.444	17.100	10.222	13.500	11.600	10.700	9.400	10.900	13.600	9.600	17.000	7.800	11.300	12.800
20.	12	27	42	57	72	87	102	117	132	147	162	177	192	207	222
21.	12.800	10.400	8.800	7.700	9.000	9.800	12.100	10.400	10.200	8.900	15.200	6.800	11.000	9.600	10.400
22.	5	20	35	50	65	80	95	110	125	140	155	170	185	200	215
23.	9.100	12.000	11.100	11.800	8.300	12.700	9.600	11.800	9.100	12.200	11.500	8.500	12.500	13.400	12.700
24.	4	19	34	49	64	79	94	109	124	139	154	169	184	199	214
25.	16.400	14.700	13.900	14.100	12.200	10.000	14.700	10.800	16.400	11.800	15.600	16.900	10.500	10.400	14.300
26.	7	22	37	52	67	82	97	112	127	142	157	172	187	202	217
27.	19.200	12.900	11.300	9.800	12.000	11.800	13.800	12.400	15.300	10.300	12.600	11.900	11.900	13.600	13.900
28.	15	30	45	60	75	90	105	120	135	150	165	180	195	210	225
29.	15.800	11.222	11.100	14.800	11.200	10.800	12.800	13.400	14.200	9.500	10.900	13.600	8.700	12.700	12.200

REPLICATION-3,

	45	59	73	87	101	115	129	143	157	171	185	199	213	2	16
1.	15.300	14.900	15.900	12.100	15.200	11.500	16.600	13.800	12.800	9.700	11.371	12.200	13.600	14.300	16.800
2.	150	164	178	192	206	220	9	23	37	51	65	79	93	107	121
	11.000	13.500	15.800	12.800	11.700	13.200	19.600	10.444	10.700	13.300	14.000	10.600	17.200	12.700	13.300
3.	90	104	118	132	146	160	174	188	202	216	5	19	33	47	61
	13.200	11.100	8.100	15.600	12.600	9.600	13.000	13.300	10.500	11.800	9.200	15.900	12.400	12.000	11.900
4.	195	209	223	12	26	40	54	68	82	96	110	124	138	152	166
	11.100	13.200	14.400	17.000	11.800	15.300	12.000	10.400	12.300	9.500	14.500	14.200	10.000	12.900	13.200
5.	105	119	133	147	161	175	189	203	217	6	20	34	48	62	76
	15.300	10.400	9.800	10.900	12.000	7.900	11.250	12.700	14.400	9.300	15.100	12.667	10.800	12.500	13.000
6.	180	194	208	222	11	25	39	53	67	81	95	109	123	137	151
	14.900	12.700	12.200	9.700	8.300	13.000	11.600	13.300	11.000	10.900	9.600	9.900	14.500	13.400	10.600
7.	60	74	88	102	116	130	144	158	172	186	200	214	3	17	31
	20.500	12.600	11.900	14.000	11.900	10.400	10.400	12.400	11.900	10.400	11.600	11.600	9.200	11.200	8.778
8.	15	29	43	57	71	85	99	113	127	141	155	169	183	197	211
	15.100	14.400	12.400	9.900	18.500	12.300	10.600	9.200	12.700	10.800	10.400	11.700	11.400	13.900	11.000
9.	225	14	28	42	56	70	84	98	112	126	140	154	168	182	196
	9.600	13.400	11.300	11.300	8.500	10.400	13.400	10.000	8.600	9.400	11.500	8.900	12.000	9.000	11.300
10.	135	149	163	177	191	205	219	8	22	36	50	64	78	92	106
	15.700	10.800	12.300	10.500	11.100	10.800	10.400	10.800	11.900	10.700	8.800	10.800	11.600	11.600	10.200
11.	165	179	193	207	221	10	24	38	52	66	80	94	108	122	136
	9.700	10.400	13.100	8.800	11.200	10.844	13.100	12.500	11.700	13.100	12.100	12.300	10.800	14.100	14.300
12.	120	134	148	162	176	190	204	218	7	21	35	49	63	77	91
	11.400	9.100	13.000	13.200	9.800	10.300	11.900	12.600	12.700	12.900	10.300	11.500	12.200	10.900	11.300
13.	30	44	58	72	86	100	114	128	142	156	170	184	198	212	1
	11.300	12.900	13.000	10.400	14.400	10.100	13.600	9.900	11.500	12.300	9.700	10.500	11.100	9.300	12.100
14.	75	89	103	117	131	145	159	173	187	201	215	4	18	32	46
	9.175	11.400	12.400	8.800	10.000	11.400	11.400	10.300	9.889	10.000	13.500	13.200	12.100	13.500	11.300
15.	212	224	13	27	41	55	69	83	97	111	125	139	153	167	181
	13.300	11.100	10.300	11.800	11.200	12.600	11.200	10.400	11.400	10.100	10.100	8.300	10.300	10.000	11.200

APPENDIX XVIII Number of spikelets per spike at Parkland

241

PARKLAND REPLICATION-1. NUMBER OF SPIKELETS PER SPIKE															
(Block)	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175
1.	11.467	12.600	13.300	13.800	13.467	13.600	14.100	14.667	13.700	12.600	14.200	12.767	13.333	11.933	14.867
2.	12.967	13.300	15.167	14.600	15.367	16.300	11.467	12.700	12.333	13.900	13.733	15.800	15.167	13.767	13.933
3.	14.533	13.067	13.133	12.433	215	216	217	218	219	220	221	222	223	224	225
4.	15.000	13.233	12.933	14.433	15.200	12.933	13.767	14.400	15.400	13.967	15.767	13.733	14.367	15.533	16.367
5.	14.630	14.567	13.667	14.600	14.533	16.167	14.900	13.667	13.267	13.133	14.633	14.900	15.100	15.933	14.133
6.	15.700	14.600	15.333	14.433	12.800	14.833	15.600	14.033	14.933	13.033	15.267	16.533	13.333	13.033	14.300
7.	14.400	12.733	16.400	14.400	12.767	14.100	15.467	14.900	14.100	13.800	12.833	14.233	11.967	14.700	12.933
8.	14.200	14.800	14.467	14.700	13.833	13.200	15.233	14.567	14.700	13.600	15.700	13.433	15.933	14.167	15.833
9.	13.600	14.767	14.700	16.067	15.000	14.667	17.600	15.500	14.200	13.433	15.567	14.200	12.867	13.467	15.367
10.	14.600	15.100	15.433	15.300	15.267	14.167	16.100	13.700	14.600	12.300	13.933	14.500	14.333	15.433	15.233
11.	15.900	14.967	16.800	13.833	14.333	14.467	15.167	12.800	14.657	14.567	206	207	208	209	210
12.	14.600	13.667	14.333	15.067	13.833	14.600	14.600	13.533	13.833	15.400	13.333	12.600	14.400	14.100	15.067
13.	15.000	14.400	13.767	14.267	14.833	14.100	14.767	15.567	14.033	10.833	13.300	13.800	16.100	15.000	15.300
14.	15.533	12.367	16.967	15.333	15.133	14.133	13.367	13.433	13.600	14.433	16.100	14.067	15.200	14.200	14.033
15.	16.300	13.933	13.800	14.800	14.100	14.733	13.433	13.800	14.067	13.867	16.633	13.900	14.733	14.935	15.467

REPLICATION-2.															
	14	29	44	59	74	89	104	119	134	149	164	179	194	209	224
1.	14.700	13.767	12.600	14.400	11.233	13.767	10.933	13.067	12.667	11.000	12.167	14.367	12.667	14.800	11.633
2.	13.300	12.133	12.933	12.567	13.600	15.267	12.233	15.200	12.300	12.667	12.567	14.933	19.033	11.900	14.867
3.	14.467	13.167	12.300	13.067	12.333	15.267	13.633	14.500	13.533	12.067	13.867	13.867	12.100	13.267	11.567
4.	14.200	13.933	13.933	13.733	13.867	12.267	14.067	15.233	13.767	15.370	13.600	11.800	11.133	12.633	13.133
5.	14.200	17.000	14.700	14.533	13.233	14.067	13.867	15.867	13.900	13.233	14.867	14.900	12.500	14.767	13.259
6.	13.800	13.367	13.933	15.033	13.833	15.267	13.300	14.800	14.767	14.000	14.833	15.900	15.300	14.967	13.433
7.	14.367	15.033	14.867	14.296	14.067	12.667	13.567	13.000	13.900	14.767	12.467	14.367	12.867	13.200	13.433
8.	12.370	13.333	12.833	15.100	13.733	13.567	13.567	14.233	12.967	14.300	15.667	13.333	13.567	14.467	13.933
9.	13.300	14.667	14.133	13.867	15.467	16.233	14.333	11.778	15.167	15.033	13.633	14.867	13.933	12.433	14.233
10.	13.222	15.593	14.133	13.963	15.533	12.467	12.900	12.800	11.833	15.600	11.567	13.933	13.767	14.333	13.933
11.	14.967	13.833	10.867	13.233	13.133	14.933	13.567	14.733	12.633	12.867	14.300	13.633	12.867	12.967	13.467
12.	14.400	14.600	14.100	13.900	13.933	15.700	13.500	15.167	15.267	13.300	14.933	13.333	13.967	14.633	12.667
13.	13.767	13.967	15.667	13.767	14.300	13.926	14.233	13.881	14.733	12.633	15.300	14.633	14.933	14.067	12.400
14.	15.167	14.133	15.133	14.000	16.367	13.633	16.933	15.900	15.600	12.800	14.967	12.700	13.300	13.433	15.267
15.	14.267	14.519	14.833	16.433	15.967	14.833	13.933	14.500	15.400	14.333	15.233	15.533	14.667	15.100	13.100

REPLICATION-3.															
	45	59	73	87	101	115	129	143	157	171	185	199	213	2	16
1.	13.667	15.367	14.067	10.833	12.000	11.433	13.333	15.067	14.067	12.200	12.874	11.000	13.767	13.133	13.833
2.	11.767	12.600	14.633	12.333	14.267	12.800	14.333	10.926	11.967	13.733	13.633	11.667	14.000	12.567	12.933
3.	12.600	13.367	13.933	14.533	13.067	11.533	14.467	11.457	13.967	13.967	12.267	14.033	19.033	11.000	11.300
4.	13.300	12.867	14.633	14.400	11.800	13.833	13.900	12.167	14.700	13.633	14.733	12.933	11.633	12.767	13.933
5.	14.300	13.500	10.767	11.333	13.633	17.433	13.458	12.767	14.167	10.667	13.900	12.037	12.500	14.267	14.567
6.	13.600	13.333	13.700	10.767	13.867	13.433	14.533	13.157	13.000	14.500	11.100	13.367	14.333	15.133	14.233
7.	15.567	13.467	14.333	13.200	13.333	13.900	14.100	17.567	13.067	12.333	14.533	10.292	13.267	13.233	11.667
8.	13.900	14.967	13.933	12.667	14.700	13.933	15.300	13.900	14.933	15.233	13.767	14.167	13.567	14.400	13.533
9.	13.900	16.533	15.833	13.300	14.933	13.500	14.467	14.867	13.700	15.033	13.267	13.967	14.333	14.033	13.933
10.	13.567	12.167	12.533	15.167	12.867	13.100	13.367	13.667	13.433	14.467	14.767	14.967	14.467	13.800	13.600
11.	13.800	14.433	14.900	14.300	12.533	14.333	14.267	15.133	12.800	13.367	13.600	14.000	12.967	15.667	13.167
12.	14.733	14.433	17.100	14.500	14.600	14.300	13.633	13.800	16.333	15.000	14.700	15.400	13.926	13.300	14.233
13.	13.833	15.067	15.033	13.300	13.767	11.433	16.600	14.100	14.333	14.967	14.133	14.947	16.067	12.667	13.733
14.	14.619	12.600	13.200	13.567	13.963	13.133	13.667	13.133	15.111	13.567	13.200	15.600	16.400	13.067	12.700
15.	13.400	12.633	12.200	13.267	12.467	13.267	11.600	12.973	16.900	15.157	14.767	14.100	12.257	14.133	12.433

APPENDIX XIX Number of seeds per spike at Parkland

		TAYLOR'S REPLICATION-1. NUMBER OF SEEDS PER SPIKE														
(Block)	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	
1.	38.267	42.600	40.867	47.300	41.913	42.531	44.167	50.000	41.300	44.733	41.267	41.200	47.400	47.267	51.033	
2.	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	
1.	47.633	47.900	48.633	44.867	43.767	51.467	43.331	39.267	37.900	44.667	51.133	49.300	46.633	46.333	46.867	
3.	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	
3.	47.533	41.067	45.100	46.867	44.433	45.567	50.233	42.833	45.533	48.200	46.767	42.300	43.600	44.533	49.567	
4.	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	
4.	46.933	43.267	47.267	44.800	49.567	39.333	45.333	45.733	44.133	43.900	55.067	40.767	45.600	46.733	49.500	
5.	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	
5.	49.000	41.733	43.333	46.733	46.633	48.367	46.900	47.233	46.067	41.867	45.067	45.767	51.100	48.167	50.467	
6.	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	
6.	53.633	45.533	47.733	48.467	48.467	44.433	48.733	50.100	50.433	45.467	48.033	50.200	44.133	47.400	44.800	
7.	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	
7.	45.833	40.133	47.100	49.600	45.133	48.967	45.633	48.233	46.400	42.833	44.867	43.700	43.267	49.967	42.267	
8.	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	
8.	41.933	48.667	50.933	51.567	45.633	47.800	46.867	46.700	46.367	40.000	49.000	47.633	50.000	45.567	58.867	
9.	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	
9.	45.900	46.367	41.833	51.367	42.800	44.967	48.867	47.467	48.800	41.700	48.567	42.200	43.000	47.400	51.500	
10.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	
10.	43.667	44.800	55.367	48.733	51.233	49.633	50.733	47.133	48.433	32.133	47.233	46.867	40.467	46.400	44.600	
11.	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	
11.	53.057	46.067	56.800	44.667	47.667	47.933	48.967	38.033	51.067	43.333	54.167	43.833	44.467	52.433	47.300	
12.	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	
12.	44.533	46.500	45.767	42.233	37.900	46.667	47.933	45.233	42.700	46.500	44.067	40.567	43.267	45.533	51.467	
13.	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	
13.	46.867	41.533	48.200	50.800	47.967	45.533	50.667	50.767	49.033	34.067	46.533	45.233	48.900	45.867	54.633	
14.	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	
14.	45.767	32.733	51.533	45.933	43.133	46.033	44.467	48.867	46.167	41.033	45.400	45.833	50.200	45.767	48.200	
15.	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	
15.	53.633	39.333	42.867	44.500	38.500	40.300	41.900	44.067	39.433	41.433	47.333	43.000	39.267	47.386	50.367	
REPLICATION-2.																
	18	29	44	59	74	89	104	119	134	149	164	179	194	209	224	
1.	44.833	44.600	41.333	42.600	35.833	49.167	39.333	42.467	43.267	40.233	44.300	46.700	42.033	45.367	40.733	
2.	1	16	31	46	61	76	91	106	121	136	151	166	181	196	211	
2.	45.100	46.167	41.800	41.667	41.400	50.867	39.200	48.400	45.433	40.767	40.833	56.000	33.757	44.300	43.867	
3.	9	24	39	54	69	84	99	114	129	144	159	174	189	204	219	
3.	48.433	41.500	42.557	41.900	38.967	44.900	43.200	44.933	47.933	39.567	50.100	42.700	41.033	45.600	41.233	
4.	2	17	32	47	62	77	92	107	122	137	152	167	182	197	212	
4.	50.900	45.067	44.700	40.133	47.400	37.167	46.533	46.267	46.767	48.593	44.167	41.367	39.800	36.333	33.600	
5.	6	21	36	51	66	81	96	111	126	141	156	171	186	201	216	
5.	52.100	55.767	49.500	47.833	46.167	49.500	48.767	51.733	45.633	43.267	46.500	48.367	43.300	45.067	47.963	
6.	11	26	41	56	71	86	101	116	131	146	161	176	191	206	221	
6.	43.933	46.800	45.700	52.633	44.167	48.300	46.400	46.367	49.533	50.433	48.267	50.300	48.233	49.767	44.800	
7.	10	25	40	55	70	85	100	115	130	145	160	175	190	205	220	
7.	42.333	52.400	50.867	46.600	41.567	40.633	41.800	47.233	43.133	45.367	40.367	44.667	40.267	43.133	54.033	
8.	8	23	38	53	68	83	98	113	128	143	158	173	188	203	218	
8.	39.185	40.633	46.600	46.333	42.333	41.900	40.100	42.367	43.900	44.633	49.100	45.933	41.967	47.367	41.467	
9.	3	18	33	48	63	78	93	108	123	138	153	168	183	198	213	
9.	49.533	44.200	45.600	47.167	50.267	45.533	47.741	36.037	42.767	45.400	40.800	43.433	44.167	41.067	53.000	
10.	13	20	43	58	73	88	103	118	133	148	163	178	193	208	223	
10.	49.111	50.444	42.000	42.444	45.600	46.200	40.300	44.833	40.133	52.467	40.800	42.300	42.467	49.567	45.567	
11.	12	27	42	57	72	87	102	117	132	147	162	177	192	207	222	
11.	50.000	45.233	35.667	44.800	45.967	47.367	46.833	45.867	45.400	47.167	45.767	39.567	39.100	39.567	41.600	
12.	5	20	35	50	65	80	95	110	125	140	155	170	185	200	215	
12.	47.300	48.500	35.733	45.900	44.900	48.967	44.300	44.833	51.533	42.067	44.467	45.200	44.733	46.033	40.100	
13.	4	19	34	49	64	79	94	109	124	139	154	169	184	199	214	
13.	47.667	41.600	47.567	42.757	46.167	46.111	39.700	46.105	46.067	44.600	49.400	47.200	48.133	46.633	44.467	
14.	7	22	37	52	67	82	97	112	127	142	157	172	187	202	217	
14.	49.667	48.200	54.400	45.267	52.800	45.667	49.900	50.267	50.867	42.433	42.767	44.133	44.600	50.433	50.533	
15.	15	30	45	60	75	90	105	120	135	150	165	180	195	210	225	
15.	42.000	42.815	50.167	48.433	47.700	48.533	42.500	46.733	49.233	47.200	49.533	49.067	49.667	45.857	42.800	
REPLICATION-3.																
	45	59	73	87	101	115	129	143	157	171	185	199	213	2	16	
1.	44.433	44.767	40.700	35.733	37.100	44.967	44.200	42.600	51.967	39.567	41.819	40.800	45.567	45.567	50.143	
2.	150	164	178	192	206	220	234	248	262	276	290	304	318	332	346	
2.	43.833	46.900	45.667	38.567	44.433	44.867	44.567	36.704	42.367	46.933	40.267	41.833	44.100	37		

APPENDIX XX Weight of seeds per spike at Parkland

243

(Block)	PARKLAND REPLICATION-1. WEIGHT OF SEEDS PER SPIKE														
	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
1.	1.367	1.611	1.569	1.725	1.669	1.766	1.505	1.905	1.654	1.758	1.496	1.804	1.749	1.434	1.637
2.	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
	1.750	1.898	1.641	1.536	1.306	1.683	1.709	1.449	1.599	1.679	2.169	1.723	1.680	1.747	1.615
3.	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225
	1.769	1.563	1.771	1.455	1.954	1.648	1.948	1.630	1.934	1.731	1.714	1.647	1.574	1.447	1.888
4.	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
	1.756	1.534	1.999	1.671	2.058	1.457	1.800	1.735	1.761	1.694	2.231	1.525	1.729	1.505	1.717
5.	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
	1.952	1.484	1.690	1.716	1.455	1.440	1.626	1.676	1.636	1.545	1.754	1.635	1.368	1.452	1.514
6.	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135
	1.648	1.697	1.732	1.715	1.771	1.479	1.756	1.961	1.937	1.480	1.625	1.771	1.694	1.841	1.634
7.	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
	1.840	1.570	1.701	1.588	1.764	1.450	1.507	1.604	1.864	1.590	1.606	1.566	1.566	1.554	1.549
8.	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
	1.520	1.553	1.753	1.826	1.773	1.645	1.765	1.720	1.724	1.351	1.705	1.618	1.494	1.511	1.971
9.	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165
	1.871	1.663	1.486	1.669	1.516	1.579	1.573	1.386	1.817	1.636	1.713	1.459	1.595	1.741	1.918
10.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
	1.695	1.744	2.114	1.590	1.992	1.641	1.565	1.818	1.495	0.812	1.793	1.539	1.606	1.313	1.632
11.	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210
	1.699	1.532	1.966	1.694	1.602	1.653	1.725	1.697	2.023	1.537	2.125	1.415	1.521	1.773	1.574
12.	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
	1.466	1.766	1.633	1.368	1.375	1.484	1.613	1.673	1.426	1.435	1.796	1.529	1.328	1.641	1.739
13.	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150
	1.854	1.485	1.819	1.809	1.676	1.703	1.870	1.695	2.076	1.127	1.649	1.472	1.393	1.544	1.965
14.	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
	1.446	1.105	1.568	1.688	1.393	1.441	1.517	1.859	1.365	1.412	1.415	1.763	1.503	1.455	1.637
15.	155	167	168	169	170	171	172	173	174	175	176	177	178	179	180
	1.719	1.554	1.382	1.624	1.134	1.772	1.645	1.740	1.321	1.386	1.629	1.535	1.451	1.657	1.628

REPLICATION-2.

1.	14	29	44	59	74	89	104	119	134	149	164	179	194	209	224
	1.362	1.669	1.509	1.504	1.175	1.931	1.398	1.490	1.281	1.416	1.556	1.641	1.308	1.522	1.554
2.	1	16	31	46	61	76	91	106	121	136	151	166	181	196	211
	1.755	1.670	1.550	1.702	1.602	1.790	1.122	1.560	1.544	1.268	1.759	1.808	1.292	1.713	1.489
3.	9	24	39	54	69	84	99	114	129	144	159	174	189	204	219
	1.336	1.941	1.661	1.306	1.475	1.626	1.573	1.372	1.876	1.691	2.110	1.443	1.532	1.521	1.453
4.	2	17	32	47	62	77	92	107	122	137	152	167	182	197	212
	2.111	1.792	1.825	1.503	1.428	1.223	1.810	1.542	1.697	1.687	1.521	1.625	1.549	1.250	1.247
5.	6	21	36	51	66	81	96	111	126	141	156	171	186	201	216
	2.178	1.976	1.807	1.723	1.855	1.911	1.983	1.689	1.601	1.752	1.382	1.463	1.710	1.520	1.849
6.	11	26	41	56	71	86	101	116	131	146	161	176	191	206	221
	1.671	1.986	2.077	1.949	1.784	1.700	1.738	1.552	1.897	2.054	1.656	1.785	1.749	1.448	1.506
7.	10	25	40	55	70	85	100	115	130	145	160	175	190	205	220
	1.820	1.823	1.687	1.524	1.455	1.429	1.494	1.896	1.506	1.667	1.604	1.672	1.468	1.337	1.730
8.	8	23	38	53	68	83	98	113	128	143	158	173	188	203	218
	1.510	1.565	1.637	1.540	1.756	1.594	1.468	1.640	1.656	1.811	1.708	1.701	1.664	1.732	1.470
9.	3	18	33	48	63	78	93	108	123	138	153	168	183	198	213
	2.051	1.722	1.960	1.927	1.861	1.529	1.683	1.463	1.513	1.649	1.486	1.789	1.511	1.520	1.930
10.	13	28	43	58	73	88	103	118	133	148	163	178	193	208	223
	1.799	1.569	1.730	1.382	1.493	1.851	1.324	1.634	1.681	1.888	1.432	1.637	1.439	1.542	1.642
11.	12	27	42	57	72	87	102	117	132	147	162	177	192	207	222
	1.558	1.723	1.269	1.802	1.895	1.733	1.781	1.680	1.756	1.880	1.777	1.304	1.095	1.438	1.855
12.	5	20	35	50	65	80	95	110	125	140	155	170	185	200	215
	1.688	1.739	1.337	1.976	1.857	1.668	1.837	1.622	1.976	1.591	1.541	1.709	1.669	1.511	1.769
13.	4	19	34	49	64	79	94	109	124	139	154	169	184	199	214
	1.613	1.447	1.657	1.325	1.924	1.764	1.435	1.668	1.566	1.700	1.612	1.716	1.590	1.727	1.437
14.	7	22	37	52	67	82	97	112	127	142	157	172	187	202	217
	1.596	1.713	2.116	1.873	1.791	1.657	1.594	1.794	1.802	1.761	1.432	1.719	1.584	1.730	1.573
15.	15	30	45	60	75	90	105	120	135	150	165	180	195	210	225
	1.472	1.524	1.872	1.693	1.683	1.900	1.417	1.705	1.885	1.875	1.980	1.698	1.849	1.632	1.593

REPLICATION-3.

	45	59	73	87	101	115	129	143	157	171	185	199	213	2	16
1.	1.402	1.252	1.366	1.055	1.262	1.435	1.545	1.602	2.022	1.530	1.639	1.519	1.631	1.993	1.899
	150	164	178	192	206	220	234	248	262	276	290	304	318	332	346
2.	1.822	1.556	1.762	1.219	1.846	1.553	1.337	1.329	1.613	1.409	1.401	1.193	1.499	1.321	1.374
	90	104	118	132	146	160	174	188	202	216	230	244	258	272	286
3.	1.673	2.064	1.993	1.840	1.792	1.573	1.265	1.705	2.130	1.490	1.715	1.613	1.268	1.471	1.166
	195	209	223	237	251	265	279	293	307	321	335	349	363	377	391
4.	1.939	1.858	1.892	1.766	1.714	1.606	1.532	1.626	1.405	1.955	1.448	1.839	1.469	1.593	1.522
	105	119	133	147	161	175	189	203	217	231	245	259	273	287	301
5.	1.550	1.752	1.403	1.374	1.545	1.705	1.964	1.667	1.426	1.458	1.095	1.119	1.546	1.263	1.440
	180	194	208	222	236	250	264	278	292	306	320	334	348	362	376
6.	1.584	1.570	1.794	1.253	1.584	1.497	1.650	1.404	1.295	1.445	1.254	1.586	1.657	1.557	1.852
	60	74	88	102	116	130	144	158	172	186	200	214	228	242	256
7.	1.597	1.875	1.649	1.600	1.811	1.251	1.717	1.603	1.685	1.638	1.753	1.140	2.084	1.721	1.703
	15	29	43	57	71	85	99	113	127	141	155	169	183	197	211
8.	1.593	1.669	1.461	1.810	1.894	1.337	1.766	1.846	1.888	1.440	1.301	1.757	1.506	1.752	1.417
	225	239	253	267	281	295	309	323	337	351	365	379	393	407	421
9.	1.646	1.783	1.655	1.541	2.128	1.481	1.357	1.861	1.637	1.766	1.653	1.754	1.644	1.871	1.624
	135	149	163	177	191	205	219	233	247	261	275	289	303	317	331
10.	1.785	1.736	1.505	2.133	1.229	1.505	1.567	2.049	1.847	1.656	1.587	1.969	1.641	1.450	1.291
	165	179	193	207	221	235	249	263	277	291	305	319	333	347	361
11.	1.497	1.711	2.028	1.350	1.456	1.537	1.734	1.600	1.676	1.659	1.299	1.553	1.381	1.712	1.523
	120	134	148	162	176	190	204	218	232	246	260	274	288	302	316
12.	1.571	1.651	1.581	1.674	1.474	1.970	1.596	1.564	1.335	1.593	1.736	1.665	1.711	1.123	2.172
	30	44	58	72	86	100	114	128	142	156	170	184	198	212	226
13.	1.710	1.557	1.741	1.620	1.480	1.426	1.591	1.809	1.605	1.739	1.677	1.649	1.834	1.374	1.691
	75	89	103	117	131	145	159	173	187	201	215	229	243	257	271
14.	1.751	1.611	1.785	1.794	1.754	1.504	1.719	1.723	1.652	1.654	1.859	1.873	1.572	1.541	1.477
	210	224	238	252	266	280	294	308	322	336	350	364	378	392	406
15.	1.712	1.527	1.534	1.818	1.473	1.434	1.639	1.676	1.792	1.737	1.994	1.750	1.395	1.634	1.572

APPENDIX XXI 1000-kernel weight at Parkland

244

PARKLAND REPLICATION-1.		1000-KERNEL WEIGHT													
(Block)	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175
1.	39.456	39.163	39.187	39.474	39.828	41.115	39.025	39.120	39.240	39.802	36.157	44.100	37.742	35.579	35.906
2.	36.363	39.581	34.032	34.363	29.749	32.705	39.553	36.786	42.639	37.592	42.061	35.004	36.026	37.431	34.563
3.	36.912	38.092	40.286	38.948	43.991	40.563	38.654	37.878	42.467	35.963	36.913	39.884	38.216	33.529	30.511
4.	37.862	35.438	42.132	36.539	41.456	36.915	38.733	38.488	35.749	38.772	40.826	37.670	37.650	31.939	34.595
5.	37.942	35.518	37.036	36.623	31.428	38.042	35.788	35.503	36.024	36.810	38.711	35.276	36.615	38.772	29.805
6.	30.711	37.209	36.352	35.184	36.641	33.357	36.354	39.150	38.528	32.834	33.863	35.332	38.318	37.689	36.564
7.	39.133	39.386	36.076	31.712	38.658	37.512	33.413	33.284	40.858	36.877	36.011	35.349	36.320	31.459	36.115
8.	34.565	31.748	34.562	35.356	38.399	34.174	37.253	35.565	37.213	33.747	34.490	33.830	29.726	33.205	33.575
9.	40.593	36.497	35.525	32.684	35.465	35.397	32.185	31.941	37.276	39.305	35.414	34.596	36.943	36.313	37.071
10.	38.818	38.423	38.018	32.559	39.639	37.097	30.685	38.546	30.855	24.353	38.149	33.136	39.249	28.876	33.305
11.	31.271	31.114	34.571	34.632	33.653	38.315	34.795	49.344	39.603	35.375	39.083	32.385	34.438	31.898	33.339
12.	31.743	37.844	35.836	32.516	36.408	31.931	31.722	36.518	33.429	31.483	40.665	37.807	30.298	36.262	34.712
13.	40.385	35.754	37.949	35.424	35.243	37.682	36.997	37.450	42.391	32.996	35.239	32.064	28.089	33.891	35.855
14.	31.523	33.697	30.437	37.219	32.262	32.229	33.703	37.694	29.084	34.640	31.176	38.325	29.921	31.743	34.665
15.	32.461	39.233	32.137	36.711	29.277	36.548	39.018	39.146	33.056	33.627	34.308	35.798	36.607	36.161	32.407

REPLICATION-2.

	18	29	44	59	74	89	104	119	134	149	164	179	194	209	224
1.	30.410	37.462	36.735	35.335	32.275	38.920	35.463	35.601	29.716	35.504	34.768	35.231	31.156	39.741	37.854
2.	40.066	40.891	38.317	40.863	38.615	35.352	28.372	32.184	33.032	30.323	43.213	32.464	37.219	38.132	29.782
3.	27.251	48.456	39.193	31.088	38.364	36.353	36.371	39.659	39.456	42.655	42.075	33.731	37.446	39.219	35.053
4.	42.059	39.835	40.740	37.323	30.154	32.963	33.892	33.471	36.095	30.412	39.362	39.866	38.558	34.975	32.448
5.	42.307	35.169	35.459	35.805	40.209	35.953	40.633	32.503	35.165	40.471	29.560	30.987	39.609	33.912	33.449
6.	37.023	42.520	45.453	37.015	40.628	34.934	37.221	33.608	38.685	40.711	33.924	35.348	35.709	37.260	32.912
7.	43.312	36.263	32.636	32.744	35.066	34.909	35.714	40.104	34.870	37.115	39.923	37.622	35.061	32.096	33.042
8.	38.168	39.271	35.394	33.233	41.124	37.147	36.651	39.055	38.257	40.066	34.619	36.858	39.420	38.698	35.005
9.	41.274	39.193	43.408	40.877	36.769	33.652	35.390	40.547	35.201	36.036	36.554	41.094	37.590	39.284	36.146
10.	36.890	30.986	41.265	33.643	32.527	40.295	32.706	36.403	41.958	36.124	30.470	38.844	33.940	31.738	36.131
11.	31.328	37.961	35.465	40.105	41.230	36.796	37.347	34.875	38.593	39.635	37.905	32.850	27.950	37.638	34.980
12.	35.415	35.824	37.470	40.609	41.617	34.312	41.687	36.785	38.394	37.932	34.756	37.739	37.732	39.354	41.873
13.	33.638	35.000	34.964	30.604	39.497	38.247	36.849	36.367	33.673	37.937	32.769	36.409	32.811	36.546	31.842
14.	31.942	35.981	38.853	41.204	33.959	36.559	32.305	35.949	35.744	41.601	33.509	39.129	34.735	35.505	31.174
15.	38.561	38.161	37.254	35.431	35.299	39.116	33.322	35.396	38.266	39.653	39.731	34.663	37.305	36.579	36.961

REPLICATION-3.

	45	59	73	87	101	115	129	143	157	171	185	199	213	2	16
1.	29.333	27.376	37.993	29.142	32.798	41.646	33.395	37.375	39.154	38.542	36.746	37.066	36.987	43.488	37.616
2.	31.900	33.359	38.517	31.532	38.726	34.617	29.844	35.545	37.800	30.121	34.862	28.352	34.038	15.213	30.198
3.	35.884	43.770	39.946	39.877	40.917	33.309	29.490	43.242	42.042	39.283	41.142	34.802	36.985	40.247	33.573
4.	38.097	40.377	40.678	34.62	26	40	54	68	82	96	110	124	138	152	166
5.	36.609	36.599	37.015	37.591	33.658	35.032	40.653	40.539	30.159	38.614	26.244	31.014	38.375	29.451	29.190
6.	37.391	38.321	39.105	36.392	32.289	33.660	37.586	32.991	32.656	30.577	36.010	35.195	33.063	32.875	39.772
7.	32.359	39.076	36.125	32.707	38.771	31.272	39.565	32.270	40.138	37.652	33.639	40.621	44.309	45.003	39.752
8.	36.806	36.423	38.660	40.417	37.207	35.724	37.454	39.795	36.296	33.993	31.108	31.880	36.472	37.846	35.302
9.	39.466	35.128	33.434	34.387	42.953	35.496	32.850	38.091	34.309	35.373	39.563	40.250	38.866	37.738	35.381
10.	38.948	46.045	39.335	45.146	35.455	38.770	40.073	41.603	39.497	34.208	36.973	39.391	35.584	35.974	28.683
11.	35.593	37.703	42.423	37.134	41.317	36.545	36.818	38.175	42.122	39.200	34.073	34.865	41.478	33.991	35.813
12.	32.899	38.201	32.421	36.045	31.452	40.405	37.235	43.542	30.384	34.741	38.740	35.844	40.010	35.413	42.571
13.	36.721	36.112	15.711	37.921	34.180	30.402	33.421	39.668	30.315	34.002	34.858	34.043	33.411	35.704	39.069
14.	34.212	35.449	39.652	35.306	39.526	37.729	37.922	40.005	35.477	37.915	42.074	36.285	34.570	37.102	38.822
15.	45.605	36.740	37.313	39.532	40.501	32.978	36.530	37.247	36.719	36.436	38.393	38.323	40.068	36.448	37.792

PARKLAND REPLICATION-1.		YIELD PER PLANT														
(Block)	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	
1.	16.580	20.177	14.075	17.342	20.463	19.037	17.917	15.448	16.826	15.351	15.272	12.253	15.034	15.218	20.657	
2.	16.563	17.710	14.230	11.598	12.388	18.533	19.534	13.081	14.654	11.957	17.183	21.111	17.129	21.231	17.689	
3.	14.819	17.194	16.325	12.107	18.705	15.975	13.061	13.136	15.370	16.062	17.581	12.395	15.006	10.704	16.749	
4.	17.735	14.602	16.437	22.993	25.119	16.181	19.494	18.625	14.499	13.572	15.876	19.980	13.054	11.662	17.969	
5.	19.323	16.326	14.620	15.365	15.666	20.425	19.028	13.881	22.244	12.811	22.498	17.755	13.697	19.786	14.818	
6.	17.626	14.547	17.918	13.929	18.042	12.603	15.563	16.677	17.742	11.257	24.775	16.783	14.219	11.739	20.342	
7.	17.435	16.774	15.853	12.695	11.989	14.332	19.093	16.183	19.131	17.975	13.630	17.621	16.513	16.644	15.203	
8.	16.622	13.126	14.093	11.261	12.692	13.889	15.214	16.357	16.329	11.753	15.075	12.153	15.268	13.727	13.379	
9.	16.847	18.819	15.531	13.550	13.630	12.400	15.095	11.936	13.724	13.731	12.459	10.344	12.291	12.729	15.185	
10.	17.991	24.412	15.671	17.135	16.116	15.239	13.083	12.760	11.759	9.114	14.020	13.206	14.743	10.201	13.809	
11.	15.111	13.532	14.043	11.775	12.103	15.456	15.271	15.815	18.219	15.033	14.470	12.732	13.159	15.619	17.844	
12.	14.891	14.139	15.922	13.761	20.220	15.105	12.550	14.827	12.010	14.419	15.564	12.645	13.340	14.596	13.430	
13.	18.536	15.197	17.751	12.945	14.314	19.289	15.771	16.795	19.377	12.595	12.631	12.652	11.714	15.990	14.456	
14.	16.698	11.514	12.614	13.453	11.723	11.529	10.703	13.785	8.256	16.869	12.563	12.602	13.696	13.468	17.802	
15.	16.174	18.162	15.547	15.809	16.147	15.555	14.267	17.357	12.310	12.727	14.267	15.801	14.195	14.839	15.006	

REPLICATION-2.

1.	9.959	12.058	16.307	14.996	8.537	17.511	10.783	16.073	11.435	10.227	11.440	12.360	10.731	13.109	11.198
2.	17.122	14.233	12.219	12.573	11.435	14.680	10.641	11.642	11.241	10.876	12.566	11.908	8.499	13.455	13.653
3.	13.507	16.042	14.350	11.931	13.158	16.555	13.506	14.242	13.328	14.156	15.470	13.267	12.359	13.430	12.572
4.	18.833	13.599	14.905	12.226	14.692	11.905	16.072	16.813	12.582	13.849	13.079	11.701	9.623	10.635	11.103
5.	15.511	16.196	12.040	14.440	12.661	15.525	11.515	14.128	12.402	11.803	13.775	11.096	10.806	18.613	13.309
6.	15.504	16.519	20.137	15.448	15.788	14.774	13.318	17.007	15.518	12.259	18.293	15.056	15.641	16.345	17.787
7.	11.975	13.834	11.355	12.217	14.660	12.433	15.693	12.244	12.774	14.671	11.770	13.062	13.845	11.162	13.725
8.	13.047	20.667	13.215	15.201	15.574	14.410	16.377	12.552	15.196	14.446	14.641	13.504	15.234	14.014	12.245
9.	16.389	14.685	13.756	20.355	19.703	13.533	14.723	12.274	13.279	15.060	12.193	15.656	11.279	18.164	17.772
10.	21.773	25.499	24.488	12.667	15.319	15.632	10.601	10.483	17.197	16.654	12.170	15.756	10.907	11.661	14.752
11.	12.420	16.496	10.172	11.586	12.265	17.433	19.314	16.657	14.219	11.653	18.595	10.276	9.679	9.838	15.280
12.	12.204	17.228	10.914	15.166	11.519	18.305	14.253	13.344	13.451	13.813	13.705	13.366	17.370	13.681	20.435
13.	15.768	13.721	15.235	12.053	18.974	12.716	19.420	13.583	13.071	13.084	16.274	18.877	12.027	11.560	13.832
14.	18.347	15.247	18.569	13.220	13.960	12.272	18.020	14.098	18.283	13.659	12.453	14.004	13.740	13.320	12.676
15.	12.805	13.277	13.426	17.429	14.026	14.450	14.888	15.745	20.405	15.582	14.928	14.097	11.200	15.403	12.714

REPLICATION-3.

1.	10.815	9.366	14.663	9.643	11.901	14.199	12.659	13.163	17.216	13.428	16.242	14.223	14.126	15.182	13.893
2.	10.611	14.538	17.881	8.940	13.582	11.691	13.065	10.868	10.747	10.138	11.513	8.191	13.452	10.862	10.089
3.	12.966	14.031	12.193	20.809	15.643	12.574	10.798	13.885	14.445	9.857	11.583	17.420	10.966	15.180	9.941
4.	14.343	18.411	15.161	15.857	13.531	16.210	11.048	13.000	11.874	14.134	12.752	17.107	13.748	14.943	13.167
5.	13.733	13.652	12.552	14.622	11.525	10.681	12.410	12.830	14.343	10.515	11.955	9.363	11.282	9.134	9.259
6.	13.440	13.742	14.915	11.907	13.720	13.261	20.095	12.073	8.953	9.413	8.208	12.033	17.601	15.739	13.343
7.	13.526	13.794	15.222	13.398	19.929	8.717	14.697	11.679	15.241	12.226	17.011	13.306	13.475	13.569	12.620
8.	12.950	13.300	13.634	13.778	17.423	14.216	14.515	12.886	15.236	10.759	11.025	16.351	12.385	19.031	14.972
9.	11.712	19.279	13.657	12.230	14.048	11.957	18.492	13.246	10.849	12.436	12.866	12.762	20.818	12.749	14.213
10.	23.854	13.200	13.798	16.590	10.759	15.293	12.555	15.078	14.376	12.382	13.848	15.047	13.458	11.031	8.530
11.	15.715	14.494	18.691	9.585	13.146	15.638	20.864	15.081	12.156	14.029	11.842	13.849	14.440	14.677	15.711
12.	15.370	10.565	13.447	13.672	12.181	13.903	17.324	15.030	11.541	15.769	12.541	12.572	11.805	10.503	17.271
13.	15.585	14.992	14.721	13.425	15.159	11.026	14.527	13.255	15.368	17.187	12.944	19.049	13.567	10.712	22.520
14.	11.130	13.595	19.455	11.931	13.909	14.946	15.040	15.174	15.163	15.625	15.541	17.787	13.055	13.031	13.621
15.	14.690	15.010	11.935	15.167	14.580	13.330	15.275	15.472	13.493	15.877	15.627	11.292	13.137	15.326	16.348

B30090